



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C12N 15/82, 15/10, 9/12, 5/10, C12Q 1/68, A01H 5/00	A2	(11) International Publication Number: WO 00/08187 (43) International Publication Date: 17 February 2000 (17.02.00)
(21) International Application Number: PCT/EP99/05652 (22) International Filing Date: 4 August 1999 (04.08.99) (30) Priority Data: 98202634.6 4 August 1998 (04.08.98) EP (71) Applicant (for all designated States except US): VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECH- NOLOGIE [BE/BE]; Rijvisschestraat 120, B-9052 Zwij- naarde (BE). (72) Inventors; and (75) Inventors/Applicants (for US only): LEE, Jeong, Hee [KR/BE]; Spinnmolenplein 274 (22K), B-9000 Gent (BE). VERBRUGGEN, Nathalie [BE/BE]; Avenue des Saisons, 53, B-1050 Ixelles (BE). (74) Agent: DE CLERCQ, Ann; Ann De Clercq & Co. B.V.B.A., Brandstraat 100, B-9830 Sint-Martens-Latem (BE).		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: GENES INVOLVED IN TOLERANCE TO ENVIRONMENTAL STRESS		
(57) Abstract <p>The present invention relates to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress resistance in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells. The present invention further relates to an isolated polynucleic acid obtainable by such a method as listed in Table 1 as well as recombinant polynucleic acid comprising the same. The present invention further relates to an isolated polypeptide encoded by a polynucleic acid of the invention. The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into a plant cell a recombinant DNA comprising a polynucleic acid as defined which when expressed in a plant cell enhances the tolerances or induces resistance to environmental stress conditions of said plant. The present invention particularly relates to plant cells, plants or harvestable parts or propagation material thereof transformed with a recombinant polynucleic acid as defined above.</p>		

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Genes involved in tolerance to environmental stress

The present invention relates to molecular biology, in particular plant
5 molecular biology. In particular, the invention relates to improvements of crop
productivity of useful plants. One of the major limitations of crop productivity is the
effect of environmental stress conditions on plant growth and development. An
important goal of molecular biology is the identification and isolation of genes that can
provide resistance or tolerance to such stresses. For agriculture, the creation of
10 transgenic plants containing such genes provides the potential for improving the stress
resistance or tolerance of plants.

Drought, salt loading, and freezing are stresses that cause adverse effects on
the growth of plants and the productivity of crops. The physiological response to these
stresses arises out of changes in cellular gene expression. Expression of a number of
15 genes has been demonstrated to be induced by these stresses (Zhu et al., 1997;
Shinozaki et al., 1996; Thomashow, 1994). The products of these genes can be
classified into two groups: those that directly protect against environmental stresses
and those that regulate gene expression and signal transduction in the stress
response. The first group includes proteins that likely function by protecting cells from
20 dehydration, such as the enzymes required for biosynthesis of various
osmoprotectants, late-embryogenesis-abundant (LEA) proteins, antifreeze proteins,
chaperones, and detoxification enzymes (Shinozaki et al., 1997, Ingram et al., 1996,
Bray et al., 1997). The second group of gene products includes transcription factors,
protein kinases, and enzymes involved in phosphoinositide metabolism (Shinozaki et
25 al., 1997). An overview of the methods known to improve stress tolerance in plants is
also given in Holmberg & Bülow, (1998).

Further studies are definitely needed to give an insight into the mechanisms
involved in the plant response to environmental stress conditions.

The study of plants naturally adapted to extreme desiccation has led to the
30 hypothesis that the genetic information for tolerance to environmental stress conditions
exists in all higher plants. In glycophytes, this information would only be expressed in
seeds and pollen grains which undergo a desiccation process.

The induction of osmotolerance in plants is very important to crop productivity:
30 to 50 % of the land under irrigation is presently affected by salinity. Several lines of
35 evidence also demonstrate that even mild environmental stress conditions throughout
the growth season have a negative impact on plant growth and crop productivity. It is

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for instance known that even minor limitations in water availability cause a reduced photosynthetic rate. Unpredictable rainfall, increase in soil salinity at the beginning and the end of the growing season often result in decreased plant growth and crop productivity. These environmental factors share at least one element of stress and that is water deficit or dehydration. Drought is a significant problem in agriculture today. Over the last 40 years, for example, drought accounted for 74% of the total US crop losses of corn. To sustain productivity under adverse environmental conditions, it is important to provide crops with a genetic basis for coping with water deficit, for example by breeding water retention and tolerance mechanisms into crops so that they can grow and yield under these adverse conditions.

It is an aim of the present invention to provide a new method for screening for plant genes involved in tolerance or resistance to environmental stress.

It is an aim of the present invention to provide new plant genes, more particularly plant genes providing the potential of improving the tolerance to environmental stress conditions in plants.

It is also an aim of the present invention to provide polypeptides encoded by said new plant genes.

It is further an aim of the present invention to provide methods for producing plants with enhanced tolerance or resistance to environmental stress conditions based on said new genes.

It is also an aim of the present invention to provide recombinant polynucleic acids comprising said new genes.

It is further an aim of the present invention to provide plant cells and plants transformed with said new genes.

It is further an aim of the present invention to provide plant cells and plants with enhanced tolerance or resistance to environmental stress conditions.

The present invention relates more particularly to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

It has been found that the transfer of genes from plants which are often difficult to assay for certain characteristics, to lower eukaryotes, such as yeasts and fungi, but

in particular yeast, especially *Saccharomyces*, is relatively-easy to achieve, whereby it has now been shown that the results of testing for tolerance or resistance to environmental conditions in the resulting yeast cells gives a relatively reliable measure of the capability of the inserted coding sequence or gene to induce tolerance or resistance to environmental stress in plants. Thus the expression of polynucleic acid sequences comprising the gene or coding sequence which are responsible for inducing tolerance or resistance to environmental stress conditions can be enhanced in the plant species from which it originates or in any other plant species.

In the present context the term "enhancing" must be understood to mean that the levels of molecules correlated with stress protection in a transformed plant cell, plant tissue or plant part will be "substantially increased" or "elevated" meaning that this level will be greater than the levels in an untransformed plant.

This may be achieved by inducing overexpression of suitable genetic information which is already present, or by any other suitable means of introducing into the plant cell heterologous information resulting in a capability to tolerate or resist environmental stress.

The term "environmental stress" has been defined in different ways in the prior art and largely overlaps with the term "osmotic stress". Holmberg et al., 1998 for instance define different environmental stress factors which result in abiotic stress. Salinity, drought, heat, chilling and freezing are all described as examples of conditions which induce osmotic stress. The term "environmental stress" as used in the present invention refers to any adverse effect on metabolism, growth or viability of the cell, tissue, seed, organ or whole plant which is produced by an non-living or non-biological environmental stressor. More particularly, it also encompasses environmental factors such as water stress (flooding, drought, dehydration), anaerobic (low level of oxygen, CO₂ etc.), aerobic stress, osmotic stress, salt stress, temperature stress (hot/heat, cold, freezing, frost) or nutrients/pollutants stress.

The term "anaerobic stress" means any reduction in oxygen levels sufficient to produce a stress as hereinbefore defined, including hypoxia and anoxia.

The term "flooding stress" refers to any stress which is associated with or induced by prolonged or transient immersion of a plant, plant part, tissue or isolated cell in a liquid medium such as occurs during monsoon, wet season, flash flooding or excessive irrigation of plants, etc.

"Cold stress" and "heat stress" are stresses induced by temperatures which are respectively, below or above, the optimum range of growth temperatures for a

particular plant species. Such optimum growth temperature ranges are readily determined or known to those skilled in the art.

“Dehydration stress” is any stress which is associated with or induced by the loss of water, reduced turgor or reduced water content of a cell, tissue, organ or whole
5 plant.

“Drought stress” refers to any stress which is induced by or associated with the deprivation of water or reduced supply of water to a cell, tissue, organ or organism.

“Oxidative stress” refers to any stress which increases the intracellular level of reactive oxygen species.

10 The terms “salinity-induced stress”, “salt-stress” or similar term refer to any stress which is associated with or induced by elevated concentrations of salt and which result in a perturbation in the osmotic potential of the intracellular or extracellular environment of a cell.

Said salt can be for example, water soluble inorganic salts such as sodium
15 sulfate, magnesium sulfate, calcium sulfate, sodium chloride, magnesium chloride, calcium chloride, potassium chloride etc., salts of agricultural fertilizers and salts associated with alkaline or acid soil conditions.

The transgenic plants obtained in accordance with the method of the present invention, upon the presence of the polynucleic acid and/or regulatory sequence
20 introduced into said plant, attain resistance, tolerance or improved tolerance or resistance against environmental stress which the corresponding wild-type plant was susceptible to.

The terms “tolerance” and “resistance” cover the range of protection from a delay to complete inhibition of alteration in cellular metabolism, reduced cell growth
25 and/or cell death caused by the environmental stress conditions defined herein before. Preferably, the transgenic plant obtained in accordance with the method of the present invention is tolerant or resistant to environmental stress conditions in the sense that said plant is capable of growing substantially normal under environmental conditions where the corresponding wild-type plant shows reduced growth, metabolism, viability,
30 productivity and/or male or female sterility. Methodologies to determine plant growth or response to stress include, but are not limited to height measurements, leaf area, plant water relations, ability to flower, ability to generate progeny and yield or any other methodology known to those skilled in the art.

The terms “tolerance” and “resistance” may be used interchangeably in the
35 present invention.

The methods according to the invention as set out below can be applied to any, higher plant, preferably important crops, preferably to all cells of a plant leading to an enhanced osmotic or any other form of environmental stress tolerance. By means of the embodiments as set out below, it now becomes possible to grow crops with improved yield, growth, development and productivity under environmental stress conditions, it may even become possible for instance to grow crops in areas where they cannot grow without the induced osmotolerance according to the invention.

In order to do a thorough screening for relevant plant genes and/or coding sequences, it is preferred to apply a method according to the invention whereby said cDNA library comprises copies of essentially all mRNA of said plant cell. Probably only coding sequences are sufficient. For the screening of genes involved in environmental stress, it is preferred to use a cDNA library from siliques (fruits, containing the maturing seeds), such as the siliques from *Arabidopsis*, because genes involved in for instance osmotolerance are preferentially expressed in these organs.

Although the genetic information may be introduced into yeast for screening by any suitable method, as long as it is in a functional format long enough for testing of tolerance or resistance to environmental stress conditions, it is preferred for ease of operation to use a well known vector such as a 2 μ plasmid. It is to be preferred to have the coding sequence or the gene under control of a strong constitutive yeast promoter, to enhance good expression of the gene or coding sequence of interest. Strong constitutive yeast promoters are well known in the art and include, but are not limited to the yeast TPI promoter.

The term "gene" as used herein refers to any DNA sequence comprising several operably linked DNA fragments such as a promoter and a 5' untranslated region (the 5'UTR), a coding region (which may or may not code for a protein), and an untranslated 3' region (3'UTR) comprising a polyadenylation site. Typically in plant cells, the 5'UTR, the coding region and the 3'UTR (together referred to as the transcribed DNA region) are transcribed into an RNA which, in the case of a protein encoding gene, is translated into a protein. A gene may include additional DNA fragments such as, for example, introns. As used herein, a genetic locus is the position of a given gene in the genome of a plant.

The present invention more particularly relates to an isolated polynucleic acid obtainable by a method comprising the preparation of a cDNA as set out above comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an

enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

The term "polynucleic acid" refers to DNA or RNA, or amplified versions thereof, or the complement thereof.

5 The present invention more particularly provides an isolated polynucleic acid obtainable by a method as defined above which encodes a polypeptide as listed in Table 1.

10 The capacity of an isolated polynucleic acid to confer tolerance or resistance to environmental stress conditions can be tested according to methods well-known in the art, see for example, Grillo et al. (1996), Peassarakli et al. (Editor), Nilsen et al. (1996), Shinozaki et al. (1999), Jones et al. (1989), Fowden et al. (1993) or as described in the appended examples.

15 The present invention more particularly relates to an isolated polynucleic acid which encodes a homolog of any of the polypeptides as listed in Table 1, which is chosen from:

- (a) any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, or 121, or the complementary strands thereof;
- 20 (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
- 25 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

30 Said fragment as defined above are preferably unique fragments of said sequences.

The term "hybridizing" refers to hybridization conditions as described in Sambrook (1989), preferably specific or stringent hybridization conditions are aimed at.

Stringent conditions are sequence dependent and will be different in different circumstances. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which
5 50% of the target sequence hybridizes to a perfectly matched probe. Typically, stringent conditions will be those in which the salt concentration is about 0.02 molar at pH 7 and the temperature is at least about 60°C.

In the present invention, genomic DNA or cDNA comprising the polynucleic acids of the invention can be identified in standard Southern blots under stringent
10 conditions using the cDNA sequence shown. The preparation of both genomic and cDNA libraries is within the skill of the art. Examples of hybridization conditions are also given in the Examples section.

The present invention also relates to the isolated polynucleic acids which encode polypeptides which are a homolog of the polypeptides as set out in Table 1
15 useful for the production of plants which are resistant or tolerant to environmental stress conditions.

The present invention also relates to a polynucleic acid comprising at least part of any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or
20 at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121. Preferably, said gene encodes a protein having
25 substantially the same biological activity as the protein having the sequence of SEQ ID NO 2, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76 or 78. Said part of said gene is preferably a unique part.

The present invention preferably relates to the use of a polynucleic acid
30 comprising at least part of any of SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%,
35 80% or 85% identical, and most preferably at least 90% or 95% identical to any of

SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121 for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

The present invention particularly relates to an isolated polynucleic acid as defined above, which encodes a plant homolog of yeast DBF2 kinase, more particularly a DBF2 kinase homolog from *Arabidopsis thaliana* termed At-DBF2, which can at least be used to confer enhanced environmental stress tolerance or resistance in plants and yeast.

More preferably, the present invention relates to an isolated polynucleic acid encoding a plant DBF2 kinase, which is chosen from:

- (a) SEQ ID NO 1, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

Alternatively, the present invention relates to a polynucleic acid derived from a plant comprising at least part of SEQ ID NO 1, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 1. Preferably said gene encodes a protein

having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2.

The present invention also relates to the use of an isolated polynucleic acid as defined above which encodes a plant HSP 17.6A protein for the production of transgenic plants, more particularly a homolog from *Arabidopsis thaliana*, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

- 10 (a) SEQ ID NO 3, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- 15 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

The present invention also relates to the use of a polynucleic acid comprising at least part of SEQ ID NO 3, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 3. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 4, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

- 35 (a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or the complementary strand thereof;

- 5
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
 - (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
 - (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

10 for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

The present invention preferably relates to the use of a polynucleic acid comprising at least part of any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more
15 preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

20 Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

25 According to another preferred embodiment, the present invention relates to an isolated polynucleic acid as defined above, which encodes a protein termed c74, more particularly a plant homolog of c74, even more preferably a c74 from *Arabidopsis thaliana*, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

More particularly, the present invention relates to an isolated polynucleic acid as defined above, which is chosen from:

30

- (a) SEQ ID NO 5, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,

5 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

10 The present invention also relates to a polynucleic acid comprising at least part of SEQ ID NO 5, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 5. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 6.

15 Two nucleic acid sequences or polypeptides are said to be "identical" according to the present invention if the sequence of nucleotides or amino acid residues, respectively, in the two sequences is the same when aligned for maximum correspondence as described below. The term "complementary to" is used herein to mean that the complementary sequence hybridizes to all or a portion of a given
20 polynucleotide sequence.

Sequence comparisons between two (or more) polynucleic acid or polypeptide sequences are typically performed by comparing sequences of the two sequences over a "comparison window" to identify and compare local regions of sequence similarity. A "comparison window", as used herein, refers to a segment of at least
25 about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman (1981), by the homology alignment
30 algorithm of Needleman and Wunsch (1970), by the search for similarity method of Pearson and Lipman (1988), by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by visual inspection.

"Percentage of sequence identity" is determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleic acid or polypeptide sequences in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not
5 comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the
10 percentage of sequence identity.

The term "substantial identity" of polynucleic acid or polypeptide sequences means that a polynucleotide sequence comprises a sequence that has at least 60%, 65%, 70% or 75% sequence identity, preferably at least 80% or 85%, more preferably at least 90% and most preferably at least 95 %, compared to a reference sequence
15 using the programs described above (preferably BLAST) using standard parameters. One of skill will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like. Substantial identity of amino acid sequences for these purposes normally means
20 sequence identity of at least 40%, 45%, 50% or 55% preferably at least 60%, 65%, 70%, 75%, 80% or 85% more preferably at least 90%, and most preferably at least 95%. Polypeptides which are "substantially similar" share sequences as noted above except that residue positions which are not identical may differ by conservative amino acid changes. Conservative amino acid substitutions refer to the interchangeability of
25 residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and
30 tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, and asparagine-glutamine.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other, or a third nucleic acid, under stringent conditions.

More particularly, the polynucleic acids as used herein will comprise at least part of a DNA sequence which is essentially similar, or, preferentially, essentially identical or identical to one or both of the nucleotide or amino acid sequences corresponding to SEQ ID NO 1 to 121 disclosed herein, more specifically in the nucleotide sequence encoding, or the amino-acid sequence corresponding to the "active domain" of the respective protein or polypeptide.

The polynucleic acid sequences according to the present invention can be produced by means of any nucleic acid amplification technique known in the art such as PCR or conventional chemical synthesis.

For a general overview of PCR see PCR Protocols (Innis et al. (1990)).

Polynucleotides may also be synthesized by well-known techniques as described in the technical literature. See, e.g., Carruthers et al. (1982) and Adams et al. (1983). Double stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

The present invention more particularly relates to an isolated polypeptide encoded by a polynucleic acid according to any of the polynucleic acids as defined above, or a functional fragment thereof.

The present invention preferably relates to an isolated polypeptide as listed in Table 1 or to an isolated polypeptide encoded by a polynucleic acid isolated as defined above. Preferably, the present invention relates to polypeptides or peptides having at least part of the sequence of any of SEQ ID NO NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Preferably, said part is a unique part and preferably includes the active domain of said polypeptide. Preferably said polypeptide is a recombinant polypeptide.

The term "isolated" distinguishes the protein or polynucleic acid according to the invention from the naturally occurring one.

The present invention also relates to a polypeptide comprising at least part of a polypeptide which is at least 50%, 55%, 60%, 65% identical, preferentially at least 70%, 75% identical, more preferably at least 80% or 85% identical, and most

preferably at least 90% or 95% identical to any of SEQ ID NO NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120.

5 The terms "polypeptide" and "protein" are used interchangeably throughout the present description.

Said polypeptide preferably has the ability to confer tolerance or resistance to environmental stress conditions in at least plants, plant parts, plant tissues, plant cells, plant calli or yeast.

10 The term "functional fragment" refers to a fragment having substantially the biological activity of the protein from which it is derived.

The polypeptides of the present invention may be produced by recombinant expression in prokaryotic and eukaryotic engineered cells such as bacteria, yeast or fungi. It is expected that those of skill in the art are knowledgeable in the numerous
15 expression systems available for expression in these systems.

The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell
20 enhances tolerance or resistance to environmental stress of said plant.

The term "plant cell" as defined above also comprises plant tissue or a plant as a whole. The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any
25 of the polynucleic acids encoding a protein as listed in Table 1 which when (over)expressed in a plant cell enhances tolerance or resistance to environmental stress in said plant.

The term "(over)expression" refers to the fact that the polypeptides of the invention encoded by said polynucleic acid are preferably expressed in an amount
30 effective to confer tolerance or resistance to the transformed plant, to an amount of salt, heat, cold, (or other stress factors) that inhibits the growth of the corresponding untransformed plant.

Several methods to obtain transient introduction and expression of a recombinant DNA in a plant are known to the art. For example, plant virus vectors can

be used to obtain such purpose. Examples conferring to the use of plant viral vectors are described in Porta and Lomonossoff (1996), WO9320217 and US 5,589,367.

The present invention also relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising stably
5 introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell enhances the environmental stress tolerance or resistance of a plant.

The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress conditions, said method
10 comprising introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids encoding a protein as listed Table 1 which when (over)expressed in a plant cell enhances the environmental stress resistance of said plant.

According to a preferred embodiment, the present invention relates to a
15 method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a DBF2 kinase, preferably a plant DBF2 kinase, most preferably an Arabidopsis DBF2 kinase.

According to another preferred embodiment, the present invention relates to a
20 method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding an HSP 17.6A protein, preferably a plant HSP 17.6A protein, most preferably an Arabidopsis HSP 17.6A.

According to a preferred embodiment, the present invention relates to a
25 method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a c74 protein, preferably a plant c74 protein, most preferably a Arabidopsis c74 protein.

Preferably, the present invention relates to a method as defined above,
30 comprising:

(a) introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:

- a polynucleic acid as defined above, and,
- a plant expressible promoter, whereby said
35 polynucleic acid is in the same transcriptional unit

and under the control of said plant-expressible promoter, and,

(b) regenerating said plant from said plant cell.

The present invention also relates to a method for producing a plant with enhanced
5 tolerance or resistance to environmental stress, said method comprising indirectly
increasing or inducing the expression of an endogenous gene in said plant comprised
within a polynucleic acid as defined above or indirectly increasing or inducing the activity
of a protein as defined above.

The present invention also relates to a method as defined above, comprising:

10 (a) introducing into the genome of a plant cell one or more recombinant DNA
molecules, said recombinant DNA molecules comprising:

- a DNA encoding a protein which when expressed in
said plant cell at an effective amount indirectly
increases or induces the expression of an
15 endogenous polynucleic acid or indirectly increases
or induces the protein activity of a protein encoded by
said polynucleic acid of the present invention, and,
- a plant expressible promoter, whereby said DNA is in
the same transcriptional unit and under the control of
20 said plant-expressible promoter, and,

(b) regenerating said plant from said plant cell.

A "recombinant" DNA molecule will comprise a "heterologous sequence"
meaning that said recombinant DNA molecule will comprise a sequence originating
from a foreign species, or, if from the same species, may be substantially modified
25 from its original form. For example, a promoter operably linked to a structural gene
which is from a species different from which the structural gene was derived, or, if
from the same species, may be substantially modified from its original form.

The present invention also relates to a method as defined above for producing
a plant with enhanced tolerance or resistance to environmental stress conditions, said
30 method comprising indirectly increasing or inducing the expression of an endogenous
gene in said plant comprised within a polynucleic acid as defined above or indirectly
increasing or inducing the activity of a protein of the invention as defined above.
According to this embodiment, other polynucleic acids modulating the expression or
the activity of a protein according to the present invention may be introduced

transiently or stably into the genome of said plants. The term "modulating" means enhancing, inducing, increasing, decreasing or inhibiting.

Increase or induction of expression or induction or increase of protein activity is required when said regulator protein is a positive regulator of the expression or the activity of at least one of the polynucleic acids or protein of the present invention.

Decrease or inhibition of expression or decrease or inhibition of protein activity is required when said regulator protein is a negative regulator of the expression or activity of at least one of the polynucleic acids or proteins of the present invention.

Increase of the activity of said polypeptide according to the present invention is obtained, according to one embodiment of the invention, by influencing endogenous gene expression in the plant. This is preferably achieved by the introduction of one or more polynucleic acid sequences according to the invention into the plant genome, in a suitable conformation for gene expression (e.g. under control of a plant-expressible promoter). This will result in increased or induced expression (overexpression) or increased or induced activity of the protein in the plant cells, and, in the presence of an adequate substrate, in an increase of tolerance or resistance to environmental stress conditions in a transgenic plant or plant cell as compared to a non-transgenic plant or plant cell. This increase in tolerance can be measured by measuring mRNA levels, or where appropriate, the level or activity of the respective protein (e.g. by means of ELISA, activity of the enzyme as measured by any technique known in the art). Endogenous gene expression refers to the expression of a protein which is naturally found in the plant, plant part or plant cell concerned.

Alternatively, said enhanced tolerance or resistance to environmental stress conditions may be achieved by introducing into the genome of the plant, one or more transgenes which interact with the expression of endogenous genes (polynucleic acids) according to the present invention, by anti-sense RNA, co-suppression or ribozyme suppression of genes which normally inhibit the expression of the polynucleic acids of the present invention or by suppression of genes which normally inhibit the activity of the polypeptides of the invention as defined above.

For inhibition of expression, the nucleic acid segment to be introduced generally will be substantially identical to at least a portion of the endogenous gene or genes to be repressed. The sequence, however, need not be perfectly identical to inhibit expression. The vectors of the present invention can be designed such that the inhibitory effect applies to other genes within a family of genes exhibiting homology or substantial homology to the target gene.

For antisense suppression, the introduced sequence also need not be full length relative to either the primary transcription product or fully processed mRNA.

Generally, higher homology can be used to compensate for the use of a shorter sequence.

5 Furthermore, the introduced sequence need not have the same intron or exon pattern, and homology of non-coding segments may be equally effective. Normally, a sequence of between about 30 or 40 nucleotides up to the full length sequence should be used, though a sequence of at least about 100 nucleotides is preferred, a sequence of at least about 200 nucleotides is more preferred, and a sequence of
10 about 500 to about 1700 nucleotides is especially preferred.

Catalytic RNA molecules or ribozymes can also be used to inhibit expression of genes as explained above. It is possible to design ribozymes that specifically pair with virtually any target RNA and cleave the phosphodiester backbone at a specific location, thereby functionally inactivating the target RNA. In carrying out this cleavage,
15 the ribozyme is not itself altered, and is thus capable of recycling and cleaving other molecules, making it a true enzyme. The inclusion of ribozyme sequences within antisense RNAs confers RNA-cleaving activity upon them, thereby increasing the activity of the constructs.

A number of classes of ribozymes have been identified. One class of
20 ribozymes is derived from a number of small circular RNAs which are capable of selfcleavage and replication in plants. The RNAs replicate either alone (viroid RNAs) or with a helper virus (satellite RNAs). Examples include RNAs from avocado sunblotch viroid and the satellite RNAs from tobacco ringspot virus, lucerne transient streak virus, velvet tobacco mottle virus, solanum nodiflorum mottle virus and
25 subterranean clover mottle virus. The design and use of target RNA-specific ribozymes is described in Haseloff et al. (1988).

Another method of suppression of gene expression is sense suppression. Introduction of nucleic acid configured in the sense orientation has been shown to be an effective means by which to block the transcription of target genes. For an example
30 of the use of this method to modulate expression of endogenous genes see, Napoli et al. (1990), and U.S. Patents Nos. 5,034,323, 5,231,020, and 5,283,184.

The suppressive effect may occur where the introduced sequence contains no coding sequence per se, but only intron or untranslated sequences homologous to sequences present in the primary transcript of the endogenous sequence. The
35 introduced sequence generally will be substantially identical to the endogenous

sequence intended to be repressed. This minimal identity will typically be greater than about 65%, but a higher identity might exert a more effective repression of expression of the endogenous sequences. Substantially greater identity of more than about 80% is preferred, though about 95% to absolute identity would be most preferred. As with
5 antisense regulation, the effect should apply to any other proteins within a similar family of genes exhibiting homology or substantial homology.

For sense suppression, the introduced sequence, needing less than absolute identity, also need not be full length, relative to either the primary transcription product or fully processed mRNA. This may be preferred to avoid concurrent production of
10 some plants which are overexpressers. A higher identity in a shorter than full length sequence compensates for a longer, less identical sequence. Furthermore, the introduced sequence need not have the same intron or exon pattern, and identity of non-coding segments will be equally effective. Normally, a sequence of the size ranges noted above for antisense regulation is used.

15 Other methods for altering or replacing genes known in the art can also be used to inhibit expression of a gene. For instance, insertional mutants using T-DNA or transposons can be generated. See, e.g., Haring et al. (1991) and Walbot (1992). Another strategy in genetic engineering of plants and animals is targeted gene replacement. Homologous recombination has typically been used for this purpose
20 (see, Capecchi (1989)).

Alternatively, the present invention also relates to a method as defined above wherein said DNA encodes a sense or antisense RNA or a ribozyme capable of indirectly increasing or inducing the expression of an endogenous polynucleic acid sequence according to the invention as defined above or increasing or inducing the
25 activity of a protein of the invention as defined above. Preferably said endogenous polynucleic acid encodes a protein as listed in Table 1.

The present invention also relates to a recombinant polynucleic acid comprising: a polynucleic acid as defined above, and, a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control
30 of said plant-expressible promoter.

The present invention also relates to a recombinant polynucleic acid comprising:

(a) a DNA encoding a protein which when expressed in said plant at an effective amount indirectly increases or induces the expression of an endogenous

polynucleic acid as defined above or indirectly increases or induces the protein activity of a polypeptide as defined above, and,

(b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

5 An "endogenous" polynucleic acid refers to a polynucleic acid that is already present in the plant species before transformation.

Said recombinant polynucleic acid as described here above is generally also referred to as a "recombinant vector" or an "expression cassette". An expression cassette of the invention can be cloned into an expression vector by standard
10 methods. The expression vector can then be introduced into host cells by currently available DNA transfer methods.

The present invention also relates to the recombinant polynucleic acid as defined above, comprising a DNA which encodes an anti-sense RNA, a ribozyme or a sense RNA which increases or induces the activity of a protein as defined above in
15 said cell. Preferably said protein is listed in Table 1.

More particularly, the present invention relates to a recombinant polynucleic acid comprising at least part of the nucleotide sequence of any of SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99,
20 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121.

Preferably, the present invention relates to a recombinant polynucleic acid comprising at least part of the coding sequence of a gene encoding a protein as listed in Table 1. Preferably, said "part" is a unique part of any of said nucleotide sequences. (26-28) As used herein, the term a "plant-expressible promoter" refers to a promoter
25 that is capable of driving transcription in a plant cell. This includes any promoter of plant origin, including the natural promoter of the transcribed DNA sequence, but also any promoter of non-plant origin which is capable of directing transcription in a plant cell. The promoter may also be an artificial or synthetic promoter. The term "plant-expressible promoter" includes, but is not restricted to, constitutive, inducible, organ-,
30 tissue-specific or developmentally regulated promoters.

According to the invention, production and/or activity of a polypeptide according to the present invention in a plant or in plant parts is increased by introducing *one or more* polynucleic acids according to the invention into the genome of the plant. More specifically, the constitutive promoter can be, but is not restricted to, one of the
35 following: a 35S promoter (Odeh et al. (1985)), a 35S'3 promoter (Hull and Howell

(1987)), the promoter of the nopaline synthase gene ("PNOS") of the Ti-plasmid (Herrera -Estrella, (1983)) or the promoter of the octopine synthase gene ("POCS", De Greve et al. (1982)). It is clear that other constitutive promoters can be used to obtain similar effects. A list of plant-expressible promoters that can be used according to the present invention is given in Table 2.

For specific embodiments of this invention, the use of inducible promoters can provide certain advantages. Modulation of protein levels or protein activity may be required in certain parts of the plant, making it possible to limit modulation to a certain period of culture or developmental stage of the plant.

For specific embodiments of this invention, the use of organ- or tissue-specific or chemical inducible promoters can provide certain advantages. Thus, in specific embodiments of the invention, the gene(s) or part thereof is (are) placed under the control of a promoter directing expression in specific plant tissues or organs, such as for instance roots, leaves, harvestable parts, etc.

It is also possible to use a promoter that can be induced upon the environmental stress conditions. Such promoters can be taken for example from stress-related genes which are regulated directly by an environmental, i.e. preferable abiotic, stress in a plant cell, including genes for which expression is increased, reduced or otherwise altered. These stress related genes comprise genes the expression of which is either induced or repressed by anaerobic stress, flooding stress, cold stress, dehydration stress, drought stress, heat stress or salinity. An exemplary list of such promoters is given in Table 3.

The recombinant polynucleic acids according to the present invention may include further regulatory or other sequences from other genes, such as leader sequences (e.g. the cab22 leader from Petunia), 3' transcription termination and polyadenylation signals (e.g. from the octopine synthase gene or the nopaline synthase gene), plant translation initiation consensus sequences, introns, transcription enhancers and other regulatory elements such as adh intron 1, etc, which is or are operably linked to the gene or a fragment thereof. Additionally, the recombinant polynucleic acid can be constructed and employed to target the gene product of the polynucleic acid of the invention to a specific intracellular compartment within a plant cell on to direct a protein to the extracellular environment. This can generally be obtained by operably joining a DNA sequence encoding a transit or signal peptide to the recombinant polynucleic acid.

The recombinant DNA comprising one or more polynucleic acids according to the present invention may be accompanied by a chimeric marker gene (Hansen et al., 1999 and references therein). The chimeric marker gene can comprise a marker DNA that is operably linked at its 5' end to a plant-expressible promoter, preferably a constitutive promoter, such as the CaMV 35S promoter, or a light inducible promoter such as the promoter of the gene encoding the small subunit of Rubisco; and operably linked at its 3' end to suitable plant transcription 3' end formation and polyadenylation signals. It is expected that the choice of the marker DNA is not critical, and any suitable marker DNA can be used. For example, a marker DNA can encode a protein that provides a distinguishable color to the transformed plant cell, such as the A1 gene (Meyer et al., (1987)), can provide herbicide resistance to the transformed plant cell, such as the *bar* gene, encoding resistance to phosphinothricin (EP 0 242 246), or can provide antibiotic resistance to the transformed cells, such as the *aac(6')* gene, encoding resistance to gentamycin (WO94/01560).

According to another embodiment, the present invention relates to the use of the polynucleic acids above as selectable marker gene. More preferably, the present invention also relates to the use of the plant DBF2 gene as defined above as selectable marker gene, selection taking place with treatment with a stress condition.

The recombinant DNA vectors according to the present invention comprising the sequences from genes of the invention will typically also comprise a marker gene which confers a selectable phenotype on plant cells. For example, the marker may encode biocide resistance, particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to chlorosulfuron or Basta.

The present invention also relates to a recombinant host cell transformed with an isolated polynucleic acid as defined above. Said host can be any host known in the art. Preferably said recombinant host cell is a plant cell, yeast, fungi, insect cell, etc. In order to be efficiently expressed in said host, said polynucleic acids can be combined with any promoter known to function in said host system. Methods for transforming said host cells are also well known in the art.

The present invention particularly also relates to a plant cell transformed with at least one recombinant polynucleic acid as defined above.

The present invention also relates to a plant consisting essentially of plant cells transformed with at least one recombinant polynucleic acid as defined above.

A "transgenic plant" refers to a plant comprising a transgene in the genome of essentially all of its cells.

DNA constructs of the invention may be introduced into the genome of the desired plant host by a variety of conventional techniques (see for example Hansen et al., 1999 for review and WO 99/05902). For example, DNA constructs of the invention may be introduced into the genome of the desired plant host by using techniques such as protoplast transformation, biolistics or microprojectile bombardment or Agrobacterium mediated transformation.

Microinjection techniques are known in the art and well described in the scientific and patent literature. The introduction of DNA constructs using polyethylene glycol precipitation is described in Paszkowski et al. (1984).

Electroporation techniques are described in Fromm et al. (1985). Biolistic transformation techniques are described in Klein et al. (1987).

Alternatively, the DNA constructs may be combined with suitable T-DNA flanking regions and introduced into a conventional Agrobacterium host vector. The virulence functions of the Agrobacterium host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria. Agrobacterium tumefaciens-mediated transformation techniques, including disarming and use of binary vectors, are well described in the scientific literature. See, for example Horsch et al. (1984), and Fraley et al. (1983).

Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype and thus the desired phenotype. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium. Plant regeneration from cultured protoplasts is described in Evans et al. (1983); and Binding (1985). Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee et al. (1987).

The polynucleic acids and polypeptides of the invention can be used to confer desired traits on a broad range of plants, including monocotyledonous or dicotyledonous plants, preferably they belong to a plant species of interest in agriculture, wood culture or horticulture, such as a crop plant, root plant, oil producing plant, wood producing plant, fruit producing plant, fodder or forage legume, companion or ornamental or horticultured plant. The plants can include species from the genera Actinidia, Apium, Allium, Ananas, Arachis, Arisaema, Asparagus, Atropa, Avena, Beta,

Brassica, Carica, Cichorium, Citrus, Citrullus, Capsicum, Cucumis, Cucurbita, Cydonia, Daucus, Diospyros, Fragaria, Glycine, Gossypium, Helianthus, Heterocallis, Hordeum, Hyoscyamus, Ipomoea, Lactuca, Linum, Lolium, Lycopersicon, Malus, Mangifera, Manihot, Majorana, Medicago, Musa, Nicotiana, Oryza, Panicum, Pannesetum, Persea, Petroselinum, Phaseolus, Pisum, Pyrus, Prunus, Raphanus, Rheum, Ribes, Rubus, Saccharum, Secale, Senecio, Sinapis, Solanum, Sorghum, Spinacia, Trigonella, Triticum, Vaccinium, Vitis, Vigna, Zea, and Zingiber. Additional species are not excluded. Crops grown on cultivated lands in arid and semi-arid areas in which irrigation with ground water is needed may advantageously benefit from the invention.

One of skill will recognize that after the recombinant polynucleic acid is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed. As described before, the plant cells, plant tissue, in particular, transgenic plants of the invention display a certain higher or enhanced degree of tolerance (or even resistance) to environmental stress conditions compared to the corresponding wild-type plants. For the meaning of "environmental stress", see supra. In a preferred embodiment of the present invention, the transgenic plant displays increased tolerance to osmotic stress, salt stress, cold and/or heat stress. An increase in tolerance to such environmental stress is understood to refer to a tolerance to a level of such stress which inhibits the growth and productivity of the corresponding untransformed plant, as determined by methodologies known to the art. Such increased tolerance in transgenic plants is related to an increased expression level in the transgenic plant or parts thereof of one or more of the polynucleic acids of the present invention and/or to an increased level of activity of the polypeptide(s) encoded by said polynucleic acid, as determined by methodologies known to the art. In comparison with their untransformed counterparts, and determined according to methodologies known in the art, a transgenic plant according to the present invention shows an increased growth, viability, metabolism, fertility and/or productivity under mild environmental stress conditions. In the alternative, a transgenic plant according to the invention can grow under environmental stress conditions wherein the untransformed counterparts can not grow. An increase in tolerance to salt stress is understood to refer to the capability of the transgenic plant to grow under stress conditions which inhibit the growth of at least 95% of the parent, non-stress tolerant plants from which the stress tolerant transgenic

plants are derived. Typically, the growth rate of stress tolerant plants of the invention will be inhibited by less than 50%, preferably less than 30%, and most preferably will have a growth rate which is not significantly inhibited by growth conditions which inhibit the growth of at least 95% of the parental, non-stress tolerant plants. In an alternative
5 example, under mild environmental stress conditions, the growth and/or productivity of the transgenic plants is statistically at least 1 % higher than for their untransformed counterparts, preferably more than 5 % higher and most preferably more than 10 % higher.

Any transformed plant obtained according to the invention can be used in a
10 conventional breeding scheme or in *in vitro* plant propagation to produce more transformed plants with the same characteristics and/or can be used to introduce the same characteristic in other varieties of the same or related species.

Furthermore, the characteristic of the transgenic plants of the present invention to maintain normal/rapid/high growth rates under environmental stress conditions can
15 be combined with various approaches to confer environmental stress tolerance with the use of other stress tolerance genes. Some examples of such stress tolerant genes are provided in Holmberg and Bülow (1998). Most prior art approaches which include the introduction of various stress tolerance genes have the drawback that they result in reduced or abnormal growth (compared to non-transgenic controls) under normal,
20 non-stressed conditions, namely stress tolerance comes at the expense of growth and productivity (Kasuga et al., 1999). This correlation between constitutive expression of stress-responsive genes and reduced growth rates under normal growth conditions indicates the presence of cross talk mechanisms between stress response control and growth control.

Furthermore, the characteristic of the transgenic plants of the present invention to display tolerance to environmental stress conditions can be combined with various
25 approaches to confer to plants other stress tolerance genes, e.g., osmotic protectants such as mannitol, proline; glycine-betaine, water-channeling proteins, etc. Thus, the approach of the present invention to confer tolerance to environmental stress
30 conditions to plants can be combined with prior art approaches which include introduction of various stress tolerance genes. Combination of these approaches may have additive and/or synergistic effects in enhancing tolerance or resistance to environmental stress.

Thus, it is immediately evident to the person skilled in the art that the method of
35 the present invention can be employed to produce transgenic stress tolerant plant with

any further desired trait (see for review TIPTEC Plant Product & Crop Biotechnology 13 (1995), 312-397) comprising:

- (i) herbicide tolerance (DE-A 3701623; Stalker (1988)),
- (ii) insect resistance (Vaek (1987)),
- 5 (iii) virus resistance (Powell (1986), Pappu (1995), Lawson (1996)),
- (iv) ozone resistance (Van Camp (1994)),
- (v) improving the preserving of fruits (Oeller (1991)),
- (vi) improvement of starch composition and/or production (Stark (1992), Visser (1991)),
- 10 (vii) altering lipid composition (Voelker (1992)),
- (viii) production of (bio)polymers (Poirer (1992)),
- (ix) alteration of the flower color, e.g., by manipulating the anthocyanin and flavonoid biosynthetic pathway (Meyer (1987), WO90/12084),
- (x) resistance to bacteria, insects and fungi (Duering (1996), Strittmatter
15 (1995), Estruch (1997)),
- (xi) alteration of alkaloid and/or cardiac glycoside composition,
- (xii) inducing maintaining male and/or female sterility (EP-A1 0 412 006; EP-A1 0 223 399; WO93/25695);
- (xiii) higher longevity of the inflorescences/flowers, and
- 20 (xvi) stress resistance.

Thus, the present invention relates to any plant cell, plant tissue, or plant which due to genetic engineering displays an enhanced tolerance or resistance to environmental stress obtainable in accordance with the method of the present invention and comprising a further nucleic acid molecule conferring a novel phenotype
25 to the plant such as one of those described above.

The present invention also relates to a callus or calli consisting essentially of plant cells as defined here above. Such transgenic calli can be preferably used for the production of secondary metabolites in plant cell suspension cultures.

The present invention also relates to any other harvestable part, organ or
30 tissue or propagation material of the plant as defined here above.

The present invention also relates to the seed of a transgenic plant as defined here above, comprising said recombinant DNA.

The present invention also relates to the use of any isolated polynucleic acid as defined above to produce transgenic plants.

The present invention also relates to the use of a recombinant polynucleic acid as defined above, to produce transgenic plants, preferably transgenic plants having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

5 The present invention also relates to the use of an isolated polynucleic acid as defined above, to produce transgenic callus having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

10 The present invention also relates to probes and primers derived from the genes of the invention that are useful for instance for the isolation of additional genes having sequences which are similar to but differ from any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, but which encode a protein
15 having substantially the same biological activity as a protein having the amino acids sequence of any of SEQ ID NO 2 to 120 (even numbers) by techniques known in the art, such as PCR. The presence of a homologous gene in another plant species can for instance be verified by means of Northern or Southern blotting experiments.

20 The present invention also relates to the cloning of the genomic counterpart of any of the cDNA sequences as represented in SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121. These genomic counterparts can be selected from a genomic library using these cDNA sequences as a probe. The present
25 invention also relates to the coding region as well as the promoter region of any of said genomic clones.

 The term "probe" according to the present invention refers to a single-stranded oligonucleotide *sequence* which is designed to specifically hybridize to any of the polynucleic acids of the invention.

30 The term "primer" refers to a single stranded oligonucleotide sequence capable of acting as a point of initiation for synthesis of a primer extension product which is complementary to the nucleic acid strand to be copied. Preferably the primer is about 5-50 nucleotides long. The term "target region" of a probe or a primer according to the present invention is a sequence within the polynucleic acid(s) to which the probe or the
35 primer is completely complementary or partially complementary (i.e. with some degree

of mismatch). It is to be understood that the complement of said target sequence is also a suitable target sequence in some cases.

"Specific hybridization" of a probe to a target region of the polynucleic acid(s) means that the probe forms a duplex with part of this region or with the entire region under the experimental conditions used, and that under those conditions this probe does substantially not form a duplex with other regions of the polynucleic acids present in the sample to be analysed.

"Specific hybridization" of a primer to a target region of the polynucleic acid(s) means that, during the amplification step, said primer forms a duplex with part of this region or with the entire region under the experimental conditions used, and that under those conditions the primer does not form a duplex with other regions of the polynucleic acids present in the sample to be analysed. It is to be understood that "duplex" as used hereby, means a duplex that will lead to specific amplification.

Preferably, the probes of the invention are about 5 nucleotides to about 1 Kb long, more preferably from about 10 to 25 nucleotides. The nucleotides as used in the present invention may be ribonucleotides, deoxyribonucleotides and modified nucleotides such as inosine or nucleotides containing modified groups which do not essentially alter their hybridization characteristics. The probes according to the present invention preferably include parts of the cDNA sequences of any of the polynucleic acids as defined above.

The present invention also relates to a composition comprising a polynucleic acid sequence as defined above, a polypeptide as defined above, a probe as defined above or a primer as defined above.

The present invention also relates to a pharmaceutical or agrochemical composition comprising said polynucleic acid, a polypeptide of the invention as defined above.

The present invention also relates to antibodies specifically reacting with a protein or polypeptide according to the present invention.

The following Examples describe by way of example the tolerance and/or resistance to several environmental stress conditions observed for transgenic plants and yeast overexpressing some of the polynucleic acids according to the present invention. Unless stated otherwise in the Examples, all recombinant DNA techniques are carried out according to standard protocols as described in Sambrook et al. (1989) and in volumes 1 and 2 of Ausubel et al. (1994). Standard materials and methods for plant molecular work are described in Plant Molecular Biology Labfax (1993) by R.D.D.

Croy, jointly published by BIOS Scientific Publications Ltd. (UK) and Blackwell Scientific Publications, UK.

These examples and figures are not to be construed as limiting to any of the embodiments of the present invention as set out above. All of the references
5 mentioned herein are incorporated by reference.

BRIEF DESCRIPTION OF THE FIGURES AND TABLES

Figure 1. *At-DBF2* encodes a functional homolog of the yeast *Dbf2* (A) Comparison of the deduced amino acid sequence of *At-DBF2* with that of yeast *DBF2*. Gaps were introduced to optimize the alignment. Roman numerals above the *At-DBF2* sequence indicate the protein kinase catalytic subdomains defined by Hanks et al. (1988). (B) Complementation of *dbf2*. The *dbf2* mutant S7-4A [*MATa dbf2Δ::URA3 ura3 leu2 ade5 trp1 his7*] (Toyn and Johnston, 1994) (B1) forms swollen pairs of daughter cells (dumbbells) at restrictive temperature (37°C). The defective morphology of the *dbf2* mutant can be complemented by transformation with the pYX112 centromeric plasmid (Ingenius, R&D system) containing the *At-DBF2* cDNA (B2) or *DBF2* (B3); wild type (CG378 strain, *MATa ade5 leu2 trp1 ura3*) (B4). Log phase cultures were shifted from 28°C to 37°C and photographed after 16 hours. After 16 hours, 98% of the S7-4A cells arrested with a dumbbell morphology (B1) whereas 6,1 and 0% of dumbbells were observed in B1, B3 and B4. Strains were kindly provided by (Dr Lindl, Max Planck Institut für Züchtungsforschung, Köln, Germany).

Figure 2. Overexpression of *DBF2* or *At-DBF2* enhances tolerance to osmotic, salt, heat and cold stress. Yeast cells were grown in YPD and cell density was adjusted to OD600 at 2. (1) DY, (2) DY transformed with pYX212 containing *DBF2*, pYX-YDBF2, (3) DY transformed with vector alone or (4) with vector containing *At-DBF2*, pYX-AtDBF2. Serial dilutions were made in step 1:10. Ten µl of each dilution was spotted on solid YPD medium (control) supplemented with 2M sorbitol (osmotic stress) or 1.2 M NaCl (salt stress) or 4µl H₂O₂ (oxidative stress) and incubated at 28°C or at 42°C (heat stress) or at 4°C (cold stress) for 3 days.

Figure 3. *DBF2* and *At-DBF2* are induced by stress. (a) Northern analysis showing the kinetics of *At-DBF2* induction in plants treated with PEG 6000 20 % and the one of *DBF2* in yeast treated with sorbitol 2M for the time indicated. (b) Northern analysis of *At-DBF2* in 10 day-old-plants grown for 5 hours in control conditions (as described in Verbruggen et al. 1993) (1), at 37°C (2), with PEG 6000 20 % (3), NaCl 1% (4), at 4°C (5) or with 0.4 mM H₂O₂ (6); and of *DBF2* in yeast cells grown for 11/2 hour in YPD (1), at 37°C (2), with sorbitol 2M (3), with NaCl 1.2 M (4), at 4°C (5) or with 0.4 mM H₂O₂ (6). Control of loading has been done with EtBr staining and is shown under each Northern analysis.

(c) Western analysis of At-DBF2 in Arabidopsis. Samples are similar to those analysed in (b). Antibodies used were raised against yeast Dbf2 and kindly provided by Dr L. Leindl (Max Planck Institut für Züchtungsforschung, Köln, Germany).

5 Figure 4. *DBF2* overexpression can suppress *hog1* osmosensitivity. The *hog1* mutant (4) [W303-1A, *MATa*, *hog1Δ::TRP1*] and wild type (W303) (1) were kindly provided by Dr Thevelein (Katholieke Universiteit Leuven, Belgium). The *hog1* mutant was transformed with pYX-YDBF2 (2) or pYX-AtDBF2 (3). Each of the 4 strains was grown for 16 hours in YPD (rich medium), and cell density was adjusted to
10 OD600 at 2. Serial dilutions, 1:10 were made at five consecutive steps. Ten microliter of each dilution was spotted on solid YPD medium (control) or solid YPD medium supplemented with 0,9 M NaCl and incubated at 28°C for 3 days.

 Figure 5. *T-DBF2* (*Nicotiana tabacum* DBF2) is periodically expressed during
15 plant cell cycle. Tobacco *DBF2* expression has been followed in BY2 cells synchronised with aphidicolin (a & b) or with propyzamide (c & d) with *At-DBF2* as probe. The measure of relative rate of DNA synthesis and of the mitotic index, the use of the cell cycle markers *CYCB1.2* and *H4* markers have been previously described (Reicheld et al., 1995). *T-DBF2* transcript levels were quantified from the blots shown
20 in b and d using a PhosphorImager (Molecular Dynamics).

 Figure 6. shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left
25 section) upon applying a salt stress of 200 mM NaCl overnight.

 Figure 7 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left
30 section) upon applying an osmotic stress induced by 20% PEG overnight.

 Figure 8 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left

section) upon applying a cold stress by gradually decreasing the temperature until – 7°C.

Figure 9 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section) upon applying a heat stress of 2 hours at 48°C.

Figure 10 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section). It can be concluded that the P35S-At-DBF2 transformed plants do not show morphological abnormalities compared to the control transgenic plants.

Figure 11 shows the results of a salt stress tolerance test with transgenic *A. thaliana* plants overexpressing HSP 17.6A (A) or c74 (B). The control plants (bottom left in A and B) is a transgenic line transformed with pBIN-35S-CaMVter. The other sections in A are 5 independently obtained transgenic lines overexpressing HSP17.6A. The other sections in B are 5 independently obtained transgenic lines overexpressing c74.

Figure 12 shows the influence of *At-DBF2* expression in sense and antisense orientations on stress tolerance. BY2 cells were transformed by *A. tumefaciens* with recombinant T-DNA vectors containing *At-DBF2* driven by CaMV 35S RNA promoter, pBIN-35S-*At-DBF2* (upper left and right sections in A or diamonds in B), the CaMV 35S promoter and terminator pBIN-35S-CaMVter (bottom left sections in A or triangles in B), or antisense *At-DBF2* under the control of the CaMV 35S promoter pBIN-35S-AS*At-DBF2* (bottom right sections in A or circles in B). (A) Picture of the same amounts of transgenic cells after 3 weeks of growth on solid medium supplemented with 300 mM NaCl, 25% PEG, 2mM H₂O₂, or at 47°C (heat). (B) Growth of suspension cells in liquid medium. Upon stress, growth was measured as fresh weight and expressed as a percentage of unstressed growth (control) (a). Stresses were applied after subculturing (= day 0) at indicated temperatures (e) and concentrations of NaCl (b) PEG (c), and H₂O₂ (f). For the cold shock (d), cells were maintained at 0°C for 2 days before the 2-week culture at 22°C. For each construction data of three

independent transgenic lines were pooled. To not overload the figure, SDs are not shown (maximum 15% of measured values). (C) Northern analysis of At-DBF2+TDBF2, kin1, and HSP17.6. Total RNAs were extracted from independent lines transformed with pBIN-35S-At-DBF2 (1) and (2), pBIN-35S-CaMter (3), and pBIN-35S-ASAt-DBF2 (4). Osmotic stress was induced with 10% PEG treatment for 5 hr (stressed).

Figure 13 shows the results of the growth of *A. thaliana* plants transformed with p35S-AtHSP17.6A and P35S control (upper right section) upon applying an osmotic stress induced by 20% PEG overnight. The results of two independent experiments are shown, each performed with 3 independently obtained transgenic lines overexpressing At-HSP17.6A (upper left and bottom left and right).

Figure 14 shows the results of the germination of *A. thaliana* plants transformed with p35S-Atc74 and P35S control (bottom section) on mineral medium supplemented with 125 mM NaCl. The results of two independent experiments are shown, each performed with 2 independently obtained transgenic lines overexpressing Atc74 (2 upper sections).

Table 1. Classification of the *Arabidopsis thaliana* clones isolated in Example 2. Clones isolated according to the description in example 2 have been analyzed on their potential to confer tolerance. According to the method described in example 2, the tolerance of different yeast transformants expressing an Arabidopsis cDNA to osmotic stress and salt stress was compared with the tolerance of DY wild type cells.

+	:	similar growth to the DY wild type cells;
++	:	growth of the transformant is visible at a 10-fold higher dilution (1:10) than control (1:1);
+++	:	growth of the transformant is visible at a 100-fold higher dilution (1:100) than control (1:1);
++++	:	growth of the transformant is visible at a 1000-fold higher dilution (1:1000) than control (1:1).

Table 2. Exemplary plant-expressible promoters for use in the performance of the present invention.

Table 3. Exemplary stress-inducible promoters for use in the performance of the present invention.

EXAMPLES

Example 1. Construction of the cDNA library.

Total RNA has been isolated from green siliques from *Arabidopsis thaliana* by grinding 1 g of siliques in 4 ml extraction buffer (100 mM tris-HCl, pH 8, 10 mM EDTA, 100 mM LiCl) at 4° C, followed by phenolisation and chloroform: isoamylalcohol (24:1) extraction. To the aqueous phase, LiCl was added up to a final concentration of 2M, and the total RNA was allowed to precipitate overnight at 4°C. After centrifugation, the pellet was redissolved in 400 µl H₂O and reprecipitated with ethanol. Poly(A) messenger RNA was isolated from the total RNA by binding it to an oligo-dT cellulose spun column (Pharmacia), washing the column three times with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA, 0.5 M NaCl and eluting the mRNA with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA at 65° C.

The eluate was precipitated with ethanol, and cDNA was synthesized using MMLV- reverse transcriptase (Pharmacia) and a d(T)₁₄-XhoI primer for the first strand and *E. coli* DNA polymerase I (Pharmacia) for the second strand.

Example 2. Yeast transformation and selection for osmotolerance.

The cDNA was cloned into pYX vectors (Ingenius, R&D systems; 2 µ based pYX 212 for bank 1, ARS/CEN based pYX112 for bank 2) as EcoRI - XhoI fragments, using an Eco RI/Not I adaptor.

In these constructs, the cDNA is under the control of the strong constitutive TPI promoter. The yeast strain DY (MATa, *his3*, *can1-100*, *ade2*, *leu2*, *trp1*, *ura3::3xSV40AP1-lacZ*; kindly provided by N. Jones, Imperial Cancer Research Fund, London, UK) has been transformed with these cDNA libraries, using the Lithium Acetate transformation procedure (Gietz and Schietsl, 1995). After transformation with the *Arabidopsis* cDNA bank, transformants have been selected for the ability to grow in the presence of 100mM LiCl in a stepwise selection (Lee et al., 1999). LiCl is commonly used for salt tolerance screening in yeast (Haro et al. 1991). Several *A. thaliana* genes, conferring osmotolerance to the yeast, have been isolated (Table 1). To further analyse the potential of the selected *Arabidopsis* cDNA's to confer tolerance to environmental stress in yeast, each yeast transformant expressing such selected *Arabidopsis* cDNA's has been exposed to osmotic stress and salt stress. Each of the transformants was therefore grown for 16 hours in YPD (rich medium), and cell density was adjusted to OD₆₀₀ at 2. Serial dilutions, 1:10, were made at three consecutive

steps. Ten microliters of each dilution was spotted on solid YPD medium (control) supplemented with 2 M sorbitol (osmotic stress) or 1.2 M NaCl (salt stress) and incubated at 28°C for 3 days. The results of this drop growth test (see also Lee et al., 1999) are shown in Table 1.

5

Example 3. Characterization of *At-DBF2*.

At-DBF2, a 1.8 kb cDNA (SEQ ID NO 1) has been identified in this screening that encodes a predicted 60.2 kDa protein showing 81 % similarity with the yeast Dbf2 transcriptional regulator. Homology (less than 40% similarity) has also been found with the putative Dbf2 homologues in human, *C. elegans* and *Drosophila* (named Ndr for nuclear Dbf2 related, Millward *et al.* 1995). The *At-DBF2* deduced protein sequence (SEQ ID NO 2) contains the 11 domains of protein kinases (Figure 1A). Amino acids lying between the invariant residues D and N of domain VI do not match the features of serine/threonine specificity (LKPE) defined by Hanks *et al.* (1988) but the GSPDYIALE peptide in domain VIII does well indicate serine/threonine specificity and *At-DBF2* can complement the yeast *dbf2* mutant (Figure 1B).

In mature *Arabidopsis* plants, *At-DBF2* is expressed in all tested organs. The highest abundance of transcripts has been found in siliques. A Southern analysis in *Arabidopsis*, tobacco and tomato has revealed that *DBF2* seems to be conserved in plants (see Example 13 below). As *At-DBF2* has been identified in a screening for LiCl tolerance, its effect in other stress situations has been tested in yeast (Figure 2).

Example 4. Overexpression of *Arabidopsis* and *Saccharomyces cerevisiae* *DBF2* enhances cold, heat, salt and drought tolerance in yeast.

In order to test whether the effect was specific to the plant gene, the yeast *DBF2* gene has been overexpressed in the same vector. Upon a drop growth test (Figure 2 and Lee et al., 1999). A remarkable enhancement of stress tolerance can be seen at 42°C, during osmotic stress (sorbitol), and after salt and cold treatments in yeast. There is no difference between stress tolerance afforded by the plant or the yeast gene. The enhancement of stress tolerance due to the overexpression of *At-DBF2* or *DBF2* reflects a role for these genes in stress situations. Therefore yeast and *Arabidopsis* plants have been exposed to sorbitol- and PEG-induced osmotic stress. *At-DBF2* as well as *DBF2* is induced rapidly (1 to 2 hours) and transiently upon osmotic stress (Figure 3A). The expression of *At-DBF2* and *DBF2* has been analyzed during other environmental stresses in *Arabidopsis* plants or in yeast cells after the

time corresponding to the highest induction seen in Fig. 3A (Figure 3B). In plant as in yeast, there is a clear induction after heat, salt, osmotic and to a lesser extent after cold, which perfectly correlates with stresses to which the overexpression enhances tolerance. However, many genes are induced upon stress without relevant adaptive role, amongst others because post-transcriptional mechanisms inhibit subsequent translation. Here *At-DBF2* protein amount, as detected by anti-Dbf2 antibodies, clearly increased upon stress (Figure 3C).

Example 5. Both *At-DBF2* and *DBF2* can functionally complement the *hog1* mutation.

To investigate a possible interaction between stress signaling pathways and *DBF2*, the salt sensitive *hog1* mutant was transformed with *At-BDF2* and *DBF2*. The *HOG1* MAP kinase pathway regulates osmotic induction of transcription in yeast (Schuller *et al.* 1994). The osmosensitivity of the mutant could be recovered by the overexpression of both *DBF2* and *At-DBF2* (Figure 4).

Example 6. *At-DBF2* is cell cycle regulated.

DBF2 expression is cell cycle regulated where it plays a role in DNA synthesis initiation but also in nuclear division through its association with the CCR4 complex (Komarnitsky *et al.* 1998, Johnston *et al.* 1990). This regulation was investigated in plants. A tobacco BY-2 cell line in which the highest level of culture synchronization, compared with other plant cell lines has been achieved so far (Shaul *et al.* 1996, Reicheld *et al.* 1995) was used. Stationary phase cells were diluted into fresh medium and treated with aphidicolin (blocking cells in the beginning of the S phase) for 24 hours, then washed. The percentage of synchronous mitosis after release from the aphidicolin block was about 65 % (Figure 5A-B). A 1.6-Kb tobacco *DBF2* homologue (*T-DBF2*) could be detected on Northern blot with the *At-DBF2* as a probe. *T-DBF2* steady-state transcript level clearly oscillates during the cell cycle and is mainly present during S, decreases during G2 until late M from where it increases until a peak in S phase. *T-DBF2* expression occurs clearly before *CYCB1.2* (a marker of G2-M phases), but parallels the one of H4 (a S phase marker) except at the S/G2 transition, where *T-DBF2* transcripts decline earlier, and at the M/G1 transition, where *T-DBF2* expression increases earlier. The use of the cell cycle markers *CYCB1.2* and H4 is described in Reicheld *et al.*

To follow unperturbed G1 and S phases, BY2 cell suspension was synchronized using a double blocking procedure (Nagata *et al.*, 1992). After the release from the aphidicoline block, cells are treated for 4 hours with propyzamide in the beginning of the preprophase. The percentage of synchronous mitosis after the release from the propyzamide block was higher than 75%. *T-DBF2* was periodically expressed with an undetectable expression until late M, a sharp increase in G1 and a peak in mid S (Figure 5C-D) which confirms results of Figures 5A-B. However a function for the plant *DBF2* in cell cycle can only be assigned with measurement of the kinase activity. In yeast, *DBF2* transcript levels do not correlate with kinase activation which occurs by dephosphorylation (Toyn and Johnson, 1994). The precise function of Dbf2 in regulation of the cell cycle is not known. An essential role has been proposed during anaphase or telophase. No activity has been measured in G1 despite evidence for a role for Dbf2 in initiation of DNA synthesis.

As other proteins recently identified, Dbf2 controls the M/G1 transition which is a major cell cycle transition in yeast (Aerne *et al.* 1998). The existence of a M/G1 control checkpoint has been suggested in plant cells (Hemmerlin and Bach 1998) but its importance compared to G1/S and G2/M has not been investigated.

Overexpression of *DBF2* in yeast results in kinase activity throughout the cell cycle, which may be due to the saturation of a post-translational deactivating mechanism (Toyn and Johnston, 1994). Overexpression of the functionally conserved *At-DBF2* has most probably the same effect. However, the presence of Dbf2 kinase activity at the wrong time in the cell cycle does apparently not affect its progression. In marked contrast constitutive activity has a marked effect on stress tolerance. The role played by *At-DBF2* or *DBF2* in stress is most probably independent from the cell division cycle. *At-DBF2* expression is present in all plant organs (abundant expression is observed in stems where only 1-2 % cells have a mitotic activity) and can be rapidly induced upon stress. However, a link with the cell cycle is not excluded. Higher stress tolerance in yeast overexpressing *DBF2* or *At-DBF2* may be correlated to the overproduction of the kinase in G1 where yeast cells are particularly sensitive to stress. Most plant cells are also thought to be blocked in G1 but the relationship with stress response is poorly known.

Example 7. Tobacco cell transformation and recombinant T-DNA Vector construction

BY2 cells were stably transformed as described (Shaul et al., 1996) by *Agrobacterium tumefaciens* C58C1Rif^R (pGV2260) strain (Deblaere et al., 1985) carrying pBIN-35S-At-DBF2 or pBIN-35S-ASAt-DBF2 recombinant binary vectors. PBIN-35S-At-DBF2 is the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the gfp reporter gene was replaced with a BamHI-SacI fragment containing the At-DBF2 cDNA from pYX-At-DBF2. p-Bin-35S-CaMVter is the plant binary vector pBIN19 in the HindIII-SacI restriction sites of which the hindIII-SacI fragment of pDH51 containing the cauliflower mosaic virus (CaMV) 35S RNA promoter and terminator was cloned. pBIN-35S-ASAt-DBF2 is the pBIN-35S-CaMVter vector in which the At-DBF2 cDNA was cloned in the antisense orientation from pYXAt-DBF2 in the BamHI-SmaI restriction sites, between the CaMV 35S RNA promoter and terminator. More details are described in Lee et al. (1999).

Example 8. Overexpression of At-DBF2 sense and antisense RNA in plant cells

Transgenic plant cells overexpressing *At-DBF2* were generated to test the role of this protein in stress tolerance *in planta*. Tobacco BY2 cells were stably transformed by *A. tumefaciens* carrying the *At-DBF2* cDNA driven by the strong constitutive CaMV 35S RNA promoter. The antisense *At-DBF2* RNA also was overexpressed under the control of the same promoter. Control lines were obtained by transforming tobacco BY2 cells with pBIN-35S-CaMVter. Three independently obtained *At-DBF2*-overexpressing tobacco transgenic cell lines have been selected with a high and similar *At-DBF2* expression and analysed further. Three tobacco transgenic cell lines overexpressing antisense *At-DBF2* were chosen that showed an undetectable tobacco DBF2 transcript level. Both the overexpression of *At-DBF2* and the down-regulation of the endogenous gene by the antisense strategy did not result in significant differences in growth after 2 weeks (Fig. 12A and 12B). On the contrary, marked differences in growth were observed after a 2-week treatment with NaCl, PEG-induced drought, cold, or high temperatures. Transgenic lines that overexpressed *At-DBF2* were clearly more tolerant than control lines. Inhibition of the endogenous DBF2 expression was correlated with a higher sensitivity to those stresses. To understand the basis of stress

tolerance in *At-DBF2*-overexpressing plant cells, expression of stress-induced genes was followed in control and stress conditions (Fig. 12C). Tobacco kin1 and HSP17.6A homologues already were induced in *At-DBF2*-overexpressing tobacco cells in control conditions to a level similar to that observed during stress conditions (PEG-induced drought), suggesting that *At-DBF2* overexpression may mimic a stress signal.

Example 9. Arabidopsis transformation and recombinant T-DNA vector construction with genes conferring tolerance to environmental stress

Arabidopsis were stably transformed as described in Clarke, Wei and Lindsey (1992) by *Agrobacterium tumefaciens* C58C1Rif^R (pGV2260) strains carrying pBIN-35S-*At-DBF2*, pBIN-35S-*At-HSP17.6A*, pBIN-35S-*At-c74* recombinant binary vectors. pBIN-35S-*At-DBF2* is described in Lee et al. 1999. pBIN-35S-*At-HSP17.6A* recombinant binary vector was constructed as following: the EcoRI-XhoI fragment containing *At-HSP17.6A* cDNA in pYX-HSP17.6A (recombinant pYX212) was first cloned in pYES2 (Invitrogen) resulting in pYES-HSP17.6A. Then the BamHI-SphI fragment of pYES-HSP17.6A containing the *At-HSP17.6A* cDNA was cloned in the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the *gfp* receptor gene was deleted and replaced by the *At-HSP17.6A* cDNA. The 3' protruding ends generated by SacI and SphI were blunt ended by T4 DNA polymerase. pBIN-35S-*c74* was constructed with a similar strategy as pBIN-35S-*AtHSP17.6A* with an intermediary pYES-*Atc74* vector. The *At-c74* cDNA was first amplified with PCR using the primers 5' AAA AAA CAC ATA CAG GAA TTC 3' (SEQ ID NO 122) and 5' AGT TAG CTA GCT GAG CTC GAG 3' (SEQ ID NO 123), then cloned "blunt ended" in the vector pYES2 cut with NotI and BstXI and blunt ended with T4 DNA polymerase. Subsequently, the BamHI-SphI fragment of pYES-*c74* was cloned in pBINm-gfp4 as explained supra.

Example 10. Tolerance to environmental stress in plant cells

Transgenic calli were isolated from each of the transgenic Arabidopsis lines transformed with *At-DBF2*, *At-HSP17.6A* and *At-c74*. The growth of these transgenic calli during salt stress was measured and compared with control calli derived from transgenic Arabidopsis lines transformed with pBIN-35S-CaMVter. Callus pieces (25 for each transgenic line) of similar fresh weight (50 to 100 mg) were therefor grown on callus inducing medium (Clarke et al., 1992) supplemented with 200mM NaCl. After two weeks, from visual inspection, it was clear that transgenic calli transformed with

At-DBF2 or At-HSP17.6A or At-c74 looked much better than control transgenic calli transformed with pBIN-35S-CaMVter. The latter calli turned yellow and started dying. To confirm the observation, the fresh weight of the calli was measured. In comparison with the control transgenic calli, the fresh weight of the transgenic calli was for each of the three lines at least five times higher than the fresh weight of the control transgenic calli.

Example 11. Tolerance to environmental stress in plants.

Seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-DBF2, p-BIN-35S-At-c74, or pBIN-35S-At-HSP17.6A, were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-AS+At-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinsteins. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 200 mM NaCl for overnight incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic lines transformed with At-DBF2 or At-HSP17.6A or At-c74 survived very well (Figure 6 and Figure 11).

To further evaluate the scope of protection to environmental stress, transgenic plants were exposed to osmotic stress. Therefor seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-DBF2, pBIN-35S-At-c74 or pBIN-35S-At-HSP17.6A were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-ASAt-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark,

70 microeinsteins. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 20 % polyethylene glycol for overnight incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic lines transformed with At-DBF2, At-HSP17.6A or At-c74 survived very well (see Figure 7 and 13). Their growth was comparable to growth on control medium without polyethylene glycol.

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to high and low temperatures. Therefor seeds from transgenic plants transformed with pBIN-35S-At-DBF2 or pBIN-35S-At-c74 were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-ASAt-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinsteins. After 9 days growth, for the experiments with high temperature stress, plants were exposed to 48°C for two hours. For the experiments with low temperature stress, plants were exposed to gradually decreasing temperatures, down to -7°C. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium.

Under both low temperature and high temperature stress, the growth of control transgenic plants was inhibited and eventually they died. The transgenic lines transformed with At-DBF2 or At-c74 survived very well. Their growth was comparable to growth under control conditions with normal temperature (see Figure 8 and 9).

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to salt stress during germination. Sterilized mature seeds from transgenic plants transformed with pBIN-35S-At-DBF2 or pBIN-35S-At-c74 were placed on top of petri dishes containing MS (Murashige and Skoog) medium with 0,8 % agar and 30 g l⁻¹ sucrose. Control plants were the ones transformed with pBIN-35S-CaMVter. Prior to germination and pH 5.7 adjustment, NaCl was added to a final concentration of 125 mM. Three petri dishes with a mean of 40-50 seeds per dish were used per treatment in every experiment. The complete experiment was repeated

twice. Seed germination at 22°C was followed. Seeds were considered to germinate after radical and green cotyledon emergency occurred.

On control medium (without 125 mM NaCl), germination of all transgenic lines was very similar to each other and to wild type plants. On medium supplemented with 125 mM NaCl, seeds from transgenic lines overexpressing At-DBF2 or At-c74 germinate significantly better than control transgenic lines. Less than 10 % of the seeds from transgenic lines transformed with pBIN-35S-CaMVter germinate under these conditions. In contrast, more than 70 % of the seeds from transgenic lines overexpressing At-DBF2 or At-c74 germinate on medium containing 125 mM NaCl (Figure 14).

Example 12. Southern hybridisation of At-DBF2 genes in other plants

To investigate whether *DBF2* homologues exist in other plant species, a Southern hybridisation analysis was performed using the full length *At-DBF2* as a probe. Genomic DNA was extracted from tobacco, tomato and rice according to Dellaporta et al. (1983) and further purified by phenol :chloroform extractions.

DNA (10 µg) was digested with restriction enzymes and separated on 1% (w/v) agarose gels using Lambda DNA digested with Hind III as molecular size standards. The DNA was transferred on to nylon membranes (Hybond N ; Amersham, little Chalfont, UK) in 0.4 N NaOH. Filters were UV-cross-linked for 30 seconds, prehybridized for 3 hours at 56°C in hybridization solution (2x SSPE, 0.1%(w/v) SDS, 5x Denhardt solution) using 200 µg/ml denatured salmon sperm DNA, and hybridized overnight with radiolabelled probes. 1X SSPE was 0.15 M NaCl/ 0.01 M sodium dihydrogen phosphate/ 1 mM EDTA

Filters were washed at 56°C in 2x SSPE, 0.1% (w/v) SDS for 20 min, then 1x SSPE, 0.1% (w/v) SDS for 20 min, and finally in 0.1x SSPE, 0.1% (w/v) SDS for 20 min. Filters were exposed to X-ray film (Kodak X-AR ; Kodak, NY, USA) in the presence of intensifying screens for 24 hours.

The results of the hybridisation experiments show that tobacco, tomato and rice have at least one homologue to At-DBF2.

Tabel 1

putative function in	Features of encoded protein	SEQ ID NO.	Growth on medium with 1,2 M NaCl	growth on medium with 2,0 M sorbitol
signalling	Similar to a yeast DBF2 cell cycle protein	1	++++	++++
metabolism	HSP17.6A	3	++++	++++
unknown	C74	5	+++	+++
metabolism	Similar to ADH2	7	+	++++
metabolism	Similar to D. melanogaster catalase/catalase 3	9	++++	+
metabolism	Similar to the HSP90 heat shock protein family	11	++++	++++
metabolism	similar to phosphoenolpyruvate carboxylase	13	+	+++
metabolism	pathogen related proteins, class 10	15	+	++++
metabolism	Arabidopsis ascorbate peroxidase	17	++++	++++
metabolism	similar to phosphatase binding protein	19	++++	++++
metabolism	similar to phosphatase binding protein	21	++++	++++
metabolism	similar to retinol dehydrogenase	23	+++	++++
metabolism	similar to retinol dehydrogenase	25	++++	++++
metabolism	ribosomal protein	27	++++	++++
metabolism	ribosomal protein	29	++++	++++
metabolism	similar to a protein transporter (kinase homolog)	31	++++	++++
metabolism	similar to a peptide transporter	33	++++	+
metabolism	similar to a wheat low affinity cation transporter LCT1	35	++++	++++
metabolism	similar to yeast iso-1-cytochrome c (CYC-1)	37	++++	++++
metabolism	similar to yeast OSM1	39	++++	++++
metabolism	similar to yeast copper uptake gene (CUP1)	41	++++	+++
metabolism	similar to yeast UV-induced damage repair protein (RAD7)	43	++++	++++
metabolism	electron transporter, apocytochrome b	45	++++	++++
metabolism	similar to membrane lipoprotein LPPL1	47	++++	++++
metabolism	similar to tobacco auxin binding protein	49	+	++++
metabolism	similar to tobacco cytokinin binding protein CBP 57	51	+++	++++
signalling	similar to calcium binding protein yeast calcineurin B	53	+++	++++

signalling	similar to calcium binding protein glycine max calnexin	55	++++	+++
signalling	similar to calcium binding protein Dictyostelium discoideum calreticulin	57	++++	++++
signalling	similar to calcium binding protein calmodulin 1	59	++++	+
signalling	similar to calcium binding protein calmodulin 2	61	+	++++
signalling	MAP kinase kinase, homologous to Dyctyostelium mekA (DdMek1)	63	++++	+++
signalling	similar to human adenosine kinase	65	+	++++
signalling	similar to human tyrosine kinase	67	++++	++++
signalling	similar to common ice plant tyrosine kinase	69	++++	++++
signalling	similar to the yeast protein kinase C receptor	71	++++	++++
signalling	similar to tobacco and Arabidopsis HAT7 homeotic protein	73	++	++++
signalling	similar to E. coli sigma factor regulator (RSEB)	75	+	++++
signalling	similar to human protein phosphatase 2C	77	++++	++++
metabolism	late embryogenesis abundant proteins, Arabidopsis LEA protein 10 & 14	79	++	++++
metabolism	late embryogenesis abundant proteins, Arabidopsis LEA protein 10 & 14	81	++	++++
metabolism	pathogen related proteins, class 10	83	++++	++++
metabolism	cell wall peroxidase	85	++++	+++
metabolism	ribosomal protein	87	+++	++++
metabolism	salt stress induced protein, SAS 1	89	++++	++++
metabolism	PR gene (AIG2)	91	++++	++++
metabolism	MT1c	93	++++	++++
metabolism	IPP2 (Isopentenyl diphosphate)	95	+++	++++
metabolism	chlorophyll a/b binding protein	97	+++	+++
metabolism	glutathione transferase	99	++	++++
signalling	cold- and ABA inducible, calcium dependent – kinase, Kin1	101	++++	++++
signalling	MAP kinase, Atmpk1	103	++	++++
signalling	Arabidopsis cell cycle protein histone H2A	105	++++	++++
unknown	chromosome 4 – sequence	107	+++	++++
unknown	chromosome 4 – sequence	109	+	++++
unknown	chromosome 5 – sequence	111	++++	+++
unknown	chromosome 5 – sequence	113	++++	++
unknown	chromosome 5 – sequence	115	++++	++++
unknown	chromosome 5 – sequence	117	+	++++
unknown	chromosome 5 – sequence	119	+	++++

signalling	similar to calcium binding protein centrin (caltractin)	121	++++	++++
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TABLE 2
EXEMPLARY PLANT-EXPRESSIBLE PROMOTERS FOR USE IN THE PERFORMANCE OF
THE PRESENT INVENTION

GENE SOURCE	EXPRESSION PATTERN	REFERENCE
α -amylase (<i>Amy32b</i>)	Aleurone	Lanahan <i>et al</i> (1992); Skriver <i>et al.</i> (1991)
cathepsin β -like gene	Aleurone	Cejudo <i>et al.</i> (1992)
<i>Agrobacterium rhizogenes</i> <i>rolB</i>	Cambium	Nilsson <i>et al.</i> (1997)
PRP genes	cell wall	http://salus.medium.edu/mmg/tierney/html
barley <i>ltr1</i> promoter	Endosperm	
synthetic promoter	Endosperm	Vicente-Carbajosa <i>et al.</i> (1998)
AtPRP4	Flowers	http://salus.medium.edu/mmg/tierney/html
chalcone synthase (<i>chsA</i>)	Flowers	van der Meer <i>et al.</i> (1990)
<i>apetala-3</i>	Flowers	
Chitinase	fruit (berries, grapes, etc)	Thomas <i>et al.</i> CSIRO Plant Industry, Urrbrae, South Australia, Australia; http://winetitles.com.au/qwrdc/csh95-1.html
<i>rbcS-3A</i>	green tissue (eg leaf)	Lam <i>et al.</i> (1990); Tucker <i>et al.</i> (1992)
leaf-specific genes	Leaf	Baszczyński <i>et al.</i> (1988)
AtPRP4	Leaf	http://salus.medium.edu/mmg/tierney/html
<i>Pinus cab-6</i>	Leaf	Yamamoto <i>et al.</i> (1994)
SAM22	Senescent leaf	Crowell <i>et al.</i> (1992)
<i>R. japonicum nif</i> gene	Nodule	United States Patent No. 4, 803, 165
<i>B. japonicum nifH</i> gene	Nodule	United States Patent No. 5, 008, 194

GmENOD40	Nodule	Yang <i>et al.</i> (1993)
PEP carboxylase (PEPC)	Nodule	Pathirana <i>et al.</i> (1992)
Leghaemoglobin (Lb)	Nodule	Gordon <i>et al.</i> (1993)
<i>Tungro bacilliform</i> virus gene	Phloem	Bhattacharyya-Pakrasi <i>et al.</i> (1992)
sucrose-binding protein gene	plasma membrane	Grimes <i>et al.</i> (1992)
pollen-specific genes	pollen; microspore	Albani <i>et al.</i> (1990); Albani <i>et al.</i> (1991)
maize pollen-specific gene	Pollen	Hamilton <i>et al.</i> (1992)
sunflower pollen-expressed gene	Pollen	Baltz <i>et al.</i> (1992)
<i>B. napus</i> pollen-specific gene	pollen; anther; tapetum	Arnoldo <i>et al.</i> (1992)
root-expressible genes	Roots	Tingey <i>et al.</i> (1987); An <i>et al.</i> (1988);
tobacco auxin-inducible gene	root tip	Van der Zaal <i>et al.</i> (1991)
β -tubulin	Root	Oppenheimer <i>et al.</i> (1988)
Tobacco root-specific genes	Root	Conkling <i>et al.</i> (1990)
<i>B. napus</i> G1-3b gene	Root	United States Patent No. 5, 401, 836
SbPRP1	Roots	Suzuki <i>et al.</i> (1993)
AtPRP1; AtPRP3	roots; root hairs	http://salus.medium.edu/mmg/tierney/html
RD2 gene	root cortex	http://www2.cnsu.edu/ncsu/research
TobRB7 gene	root vasculature	http://www2.cnsu.edu/ncsu/research
AtPRP4	leaves; flowers; lateral root primordia	http://salus.medium.edu/mmg/tierney/html
Seed-specific genes	Seed	Simon <i>et al.</i> (1985); Scofield <i>et al.</i> (1987); Baszczynski <i>et al.</i> (1990)
Brazil Nut albumin	seed	Pearson <i>et al.</i> (1992)
Legumin	Seed	Ellis <i>et al.</i> (1988)
Glutelin (rice)	Seed	Takaiwa <i>et al.</i> (1986); Takaiwa <i>et al.</i>

		(1987)
Zein	Seed	Matzke <i>et al.</i> (1990)
NapA	Seed	Stalberg <i>et al.</i> (1996)
Sunflower oleosin	seed(embryo and dry seed)	Cummins <i>et al.</i> (1992)
<i>LEAFY</i>	shoot meristem	Weigel <i>et al.</i> (1992)
<i>Arabidopsis thaliana knat1</i>	shoot meristem	Accession number AJ131822
<i>Malus domestica kn1</i>	shoot meristem	Accession number Z71981
<i>CLAVATA1</i>	shoot meristem	Accession number AF049870
Stigma-specific genes	Stigma	Nasrallah <i>et al.</i> (1988); Trick <i>et al.</i> (1990)
Class I patatin gene	Tuber	Liu <i>et al.</i> (1991)
<i>Blz2</i>	Endosperm	EP99106056.7
PCNA rice	Meristem	Kosugi <i>et al.</i> (1991); Kosugi and Ohashi (1997)

Table 3. Stress inducible promoters

Name	Stress	Reference
P5CS (delta(1)-pyrroline-5-carboxylate syntase)	salt, water	Zhang et al; Plant Science. Oct 28 1997; 129(1): 81-89
cor15a	Cold	Hajela et al., Plant Physiol. 93: 1246-1252 (1990)
cor15b	Cold	Wlihelm et al., Plant Mol Biol. 1993 Dec; 23(5):1073-7
cor15a (-305 to +78 nt)	cold, drought	Baker et al., Plant Mol Biol. 1994 Mar; 24(5): 701-13
rd29	salt, drought, cold	Kasuga et al., Nature Biotechnology, vol 18, 287-291, 1999
heat shock proteins, including artificial promoters containing the heat shock element (HSE)	Heat	Barros et al., Plant Mol Biol, 19(4): 665-75, 1992. Marrs et al., Dev Genet., 14(1): 27-41, 1993. Schoffl et al., Mol Gen Gent, 217(2-3): 246-53, 1989.
smHSP (small heat shock proteins)	heat	Waters et al, J Experimental Botany, vol 47, 296, 325-338, 1996
wcs120	Cold	Ouellet et al., FEBS Lett. 423, 324-328 (1998)
ci7	Cold	Kirch et al., Plant Mol Biol, 33(5): 897-909, 1997 Mar
Adh	cold, drought, hypoxia	Dolferus et al., Plant Physiol, 105(4): 1075-87, 1994 Aug
pws18	water: salt and drought	Joshee et al., Plant Cell Physiol, 39(1): 64-72, 1998, Jan
ci21A	Cold	Schneider et al., Plant Physiol, 113(2): 335-45, 1997
Trg-31	Drought	Chaudhary et al., Plant Mol Biol, 30(6): 1247-57, 1996
Osmotin	Osmotic	Raghothama et al., Plant Mol Biol, 23(6): 1117-28, 1993

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Claims

1. A method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.
2. An isolated polynucleic acid obtainable by a method according to claim 1.
3. The isolated polynucleic acid of claim 2 which encodes a polypeptide as listed in Table 1.
4. The isolated polynucleic acid of claim 3, which is chosen from:
 - (a) any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or the complementary strands thereof;
 - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
 - (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
 - (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).
5. The isolated polynucleic acid of any of claim 2 to 4, which encodes a plant homolog of yeast DBF2 kinase.
6. The isolated polynucleic acid of claim 5, which is chosen from:
 - (a) SEQ ID NO 1, or the complementary strands thereof;
 - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

5

7. Use of an isolated polynucleic acid of claims 2 to 3 which encodes an HSP 17.6A protein for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

- 10 8. Use of an isolated polynucleic acid of claim 7 for expression of the protein encoded thereby in a plant cell, with said polynucleic acid being chosen from:

- (a) SEQ ID NO 3, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- 15 (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of
- 20 (a) to (c).

9. Use of an isolated polynucleic acid as defined above which is chosen from:

- (a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or the complementary strand thereof;
- 25 (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- 30 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

for the production of transgenic plants having an enhanced tolerance or resistance to
35 environmental stress conditions.

10. The isolated polynucleic acid of any of claims 2 to 4, which encodes a c74 protein which is chosen from:
- (a) SEQ ID NO 5, or the complementary strand thereof;
 - 5 (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
 - (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
 - 10 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).
11. An isolated polypeptide encoded by a polynucleic acid according to or as defined
- 15 in any of claims 2 to 10, or a functional fragment thereof.
12. The isolated polypeptide of claim 11 having at least part of the sequence of any of SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84,
- 20 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120.
13. A method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising transiently introducing into a plant
- 25 cell a recombinant DNA comprising a polynucleic acid of or as defined in any of claims 2 to 10 which is expressed in an amount effective to confer enhanced tolerance or resistance to environmental stress.
14. A method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising stably introducing into a plant cell a
- 30 recombinant DNA comprising a polynucleic acid of or as defined in any of claims 2 to 10 which is expressed in an amount effective to confer enhanced tolerance or resistance to environmental stress.

15. The method of claims 13 or 14 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claims 5 or 6 encoding a plant DBF2 kinase.
- 5 16. The method of claim 16 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claims 7 or 8 encoding an HSP 17.6A protein.
- 10 17. The method of claim 13 to 14 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claim 10 encoding a c74 protein.
- 15 18. The method of any of claims 13 to 17, comprising introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:
- a polynucleic acid according to or as defined in any of claims 2 to 10, and,
 - a plant expressible promoter, whereby said
- 20 polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.
- 25 19. A method for producing a plant with enhanced tolerance or resistance to environmental stress, comprising introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:
- a DNA encoding a protein which when expressed in said plant cell at an effective amount indirectly increases or induces the expression of an
- 30 endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or indirectly increases or induces the activity of a polypeptide of claims 11 or 12, and,

- a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

5 20. A method of claim 19 wherein said DNA encodes a sense or antisense RNA molecule or a ribozyme capable of increasing or inducing the expression of said endogenous polynucleic acid sequence according to or as defined in any of claims 2 to 10.

10 21. A recombinant polynucleic acid comprising:
a polynucleic acid according to or as defined in any of claims 2 to 10, and,
a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.

15 22. A recombinant polynucleic acid comprising:
(a) a DNA encoding a protein which when expressed in said plant cell at an effective amount increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or increases or induces the activity of a polypeptide of claims 11 or 12, and,
20 (b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

23. The recombinant polynucleic acid of claim 22, wherein said DNA encodes an anti-sense RNA, a ribozyme or a sense RNA which when expressed in a cell of a plant
25 increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or which induces or increases the activity of a protein of claim 11 or 12.

24. The recombinant polynucleic acid of claim 21 comprising at least part of the
30 nucleotide sequence of any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or part thereof.

25. The recombinant polynucleic acid of claim 21 to 24 comprising at least part of the coding sequence of a gene encoding a protein as listed in Table 1.
26. The recombinant polynucleic acid of any of claims 21 to 25 wherein said plant-expressible promoter is a constitutive promoter.
27. The recombinant polynucleic acid of any of claims 21 to 25 wherein said plant-expressible promoter is a stress-inducible or organ- or tissue-specific promoter.
28. The recombinant polynucleic acid of any of claims 21 to 26 wherein said plant-expressible promoter is the 35S promoter of CaMV.
29. A recombinant host cell transformed with at least one isolated polynucleic acid of or as defined in any of claims 2 to 10.
30. A plant cell transformed with a recombinant polynucleic acid of any one of claims 21 to 28.
31. A plant consisting essentially of plant cells of claim 30.
32. A callus consisting essentially of plant cells of claim 30.
33. A harvestable part, organ, tissue or propagation material of a plant of claim 31, comprising said recombinant DNA.
34. The use of a recombinant polynucleic acid of claim 21 to 28 to produce transgenic plants.
35. A probe which is part of the polynucleic acid sequence of or as defined in any of claims 2 to 10 and which hybridizes specifically with said polynucleic acid or the complement thereof.
36. A primer which is part of the polynucleic acid sequence of or as defined in any of claims 2 to 10 and which specifically amplifies said polynucleic acid or the complement thereof.

37. A composition comprising a polynucleic acid sequence of or as defined in any of claims 2 to 10, a polypeptide of claim 11 or 12, a probe of claim 35 or a primer of claim 36.

FIGURE 1 A

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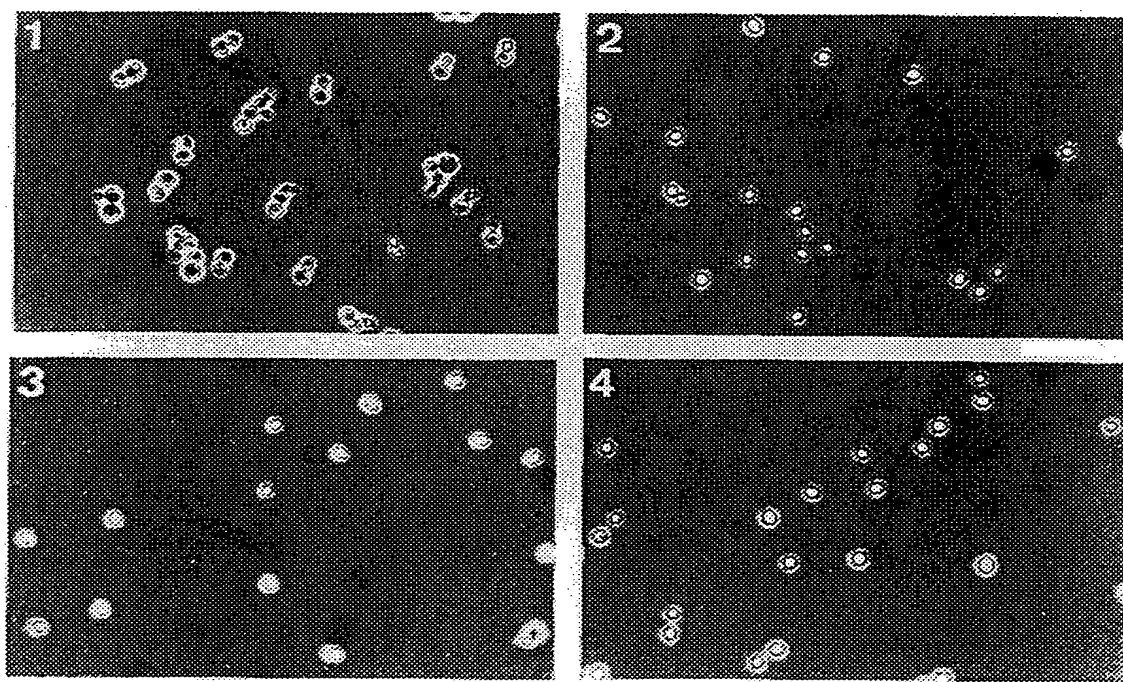


FIGURE 1B

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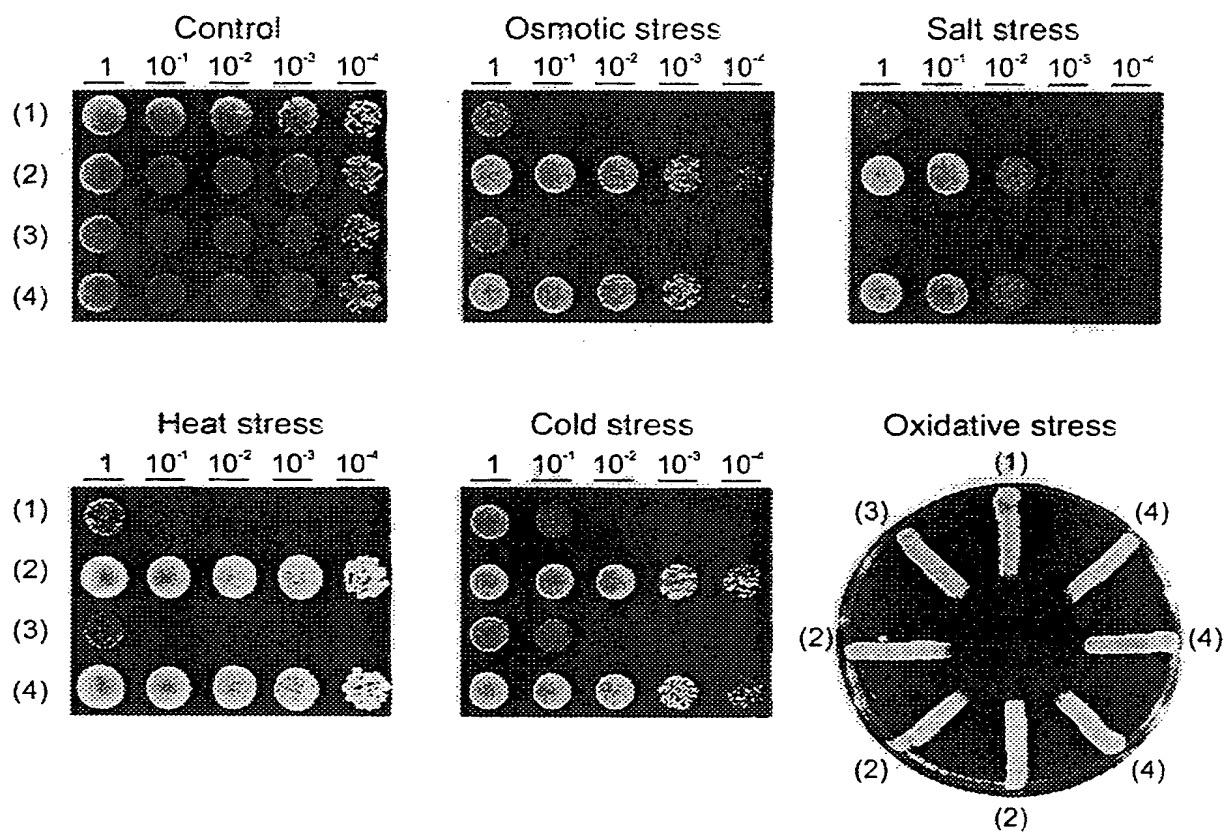


FIGURE 2

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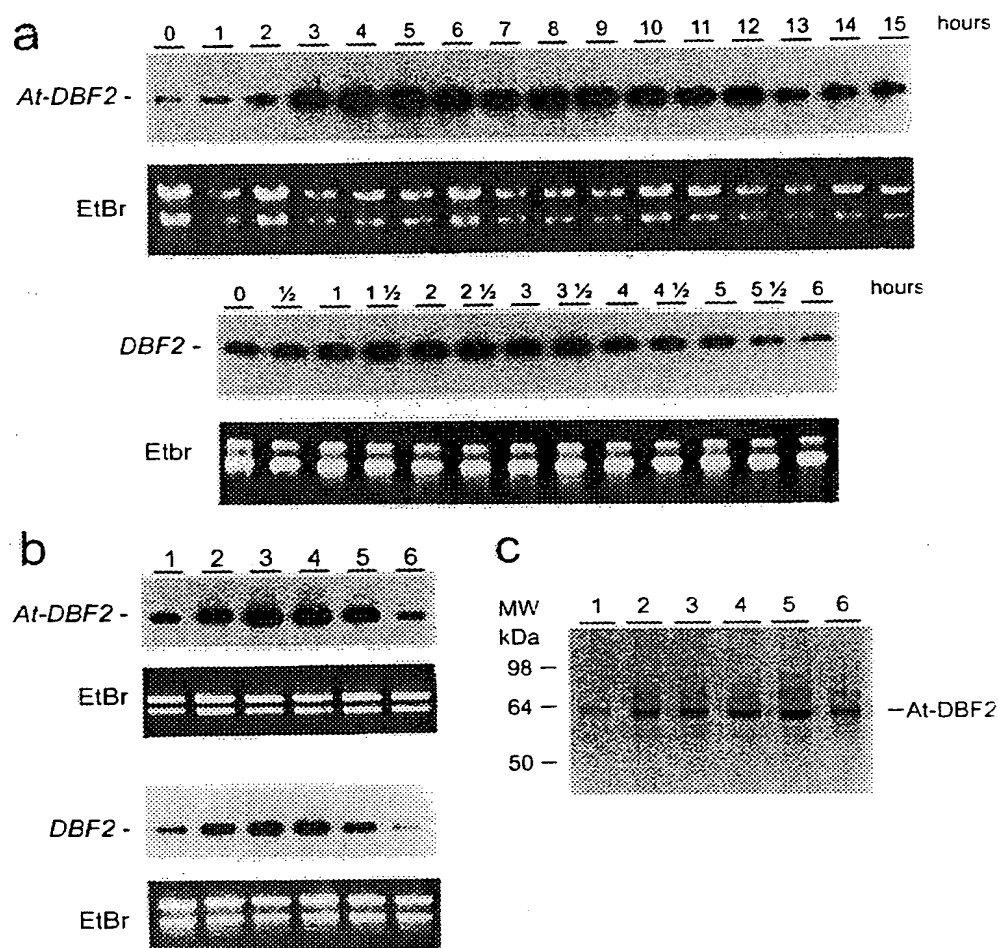


FIGURE 3

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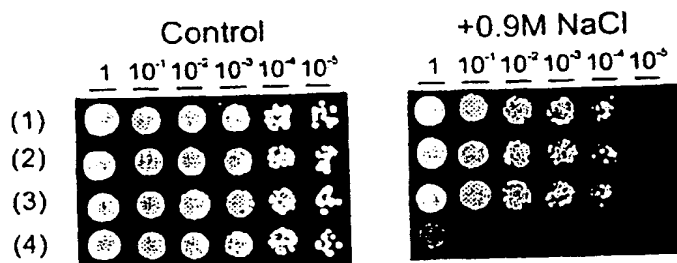


FIGURE 4

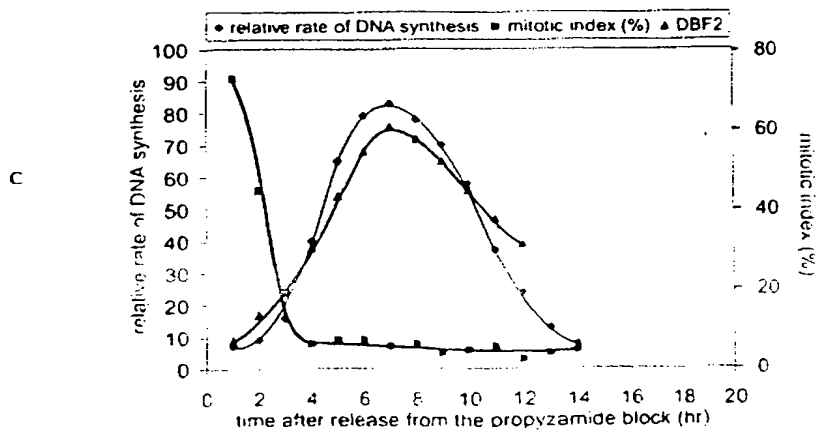
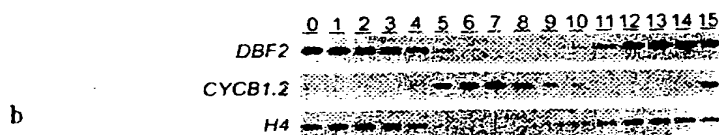
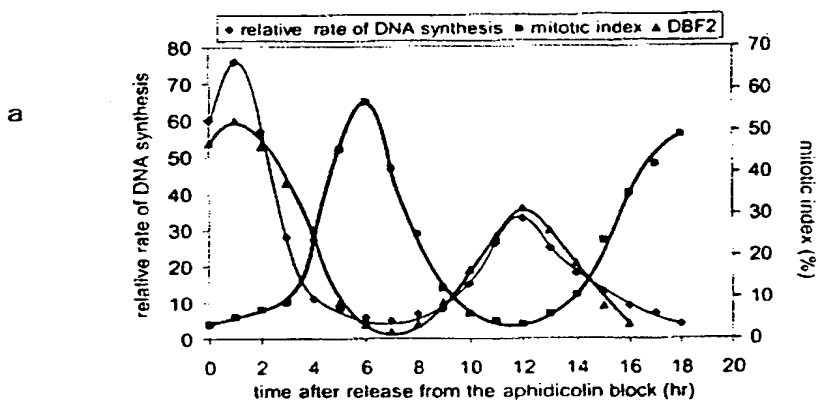


FIGURE 5

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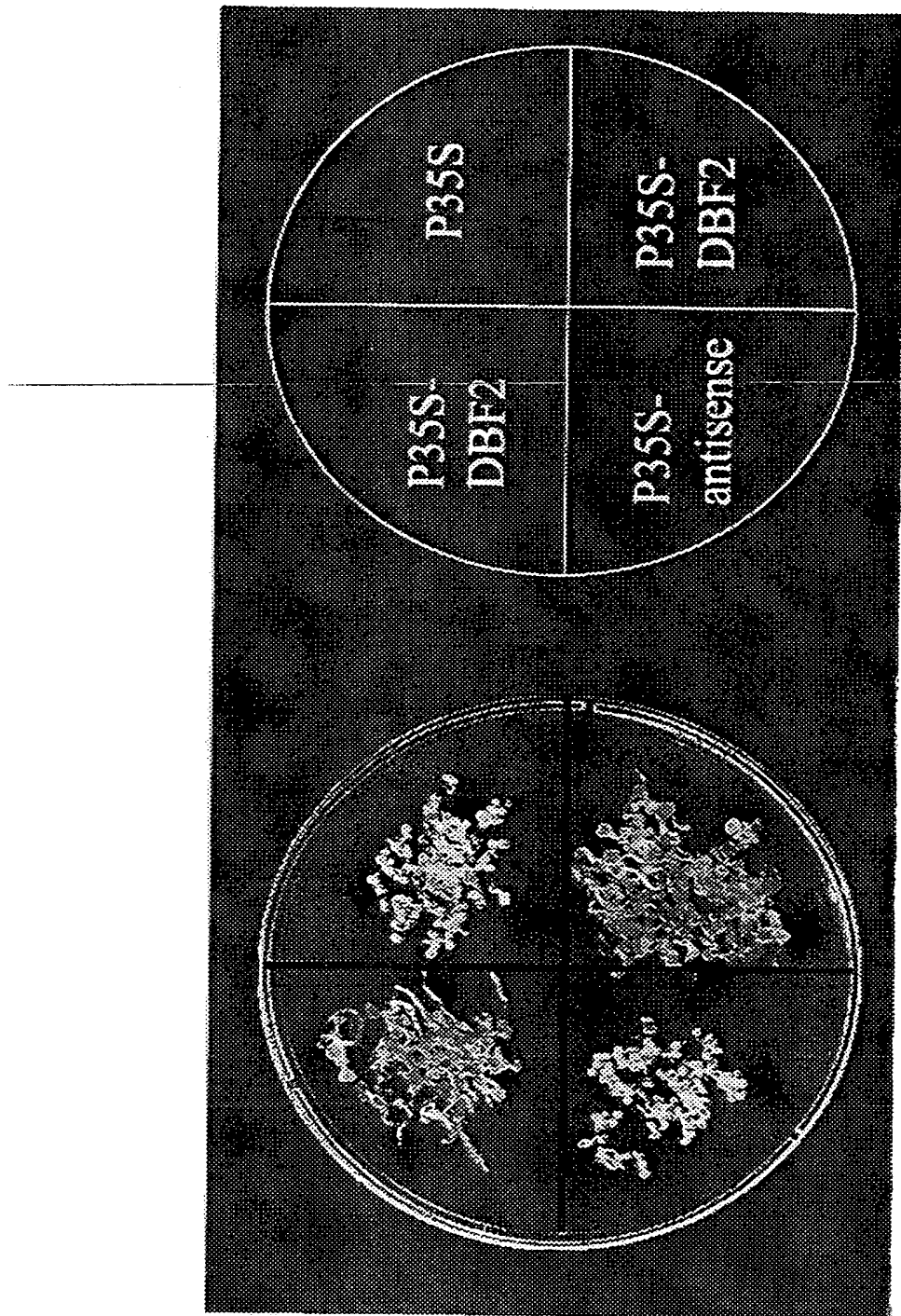


FIGURE 6

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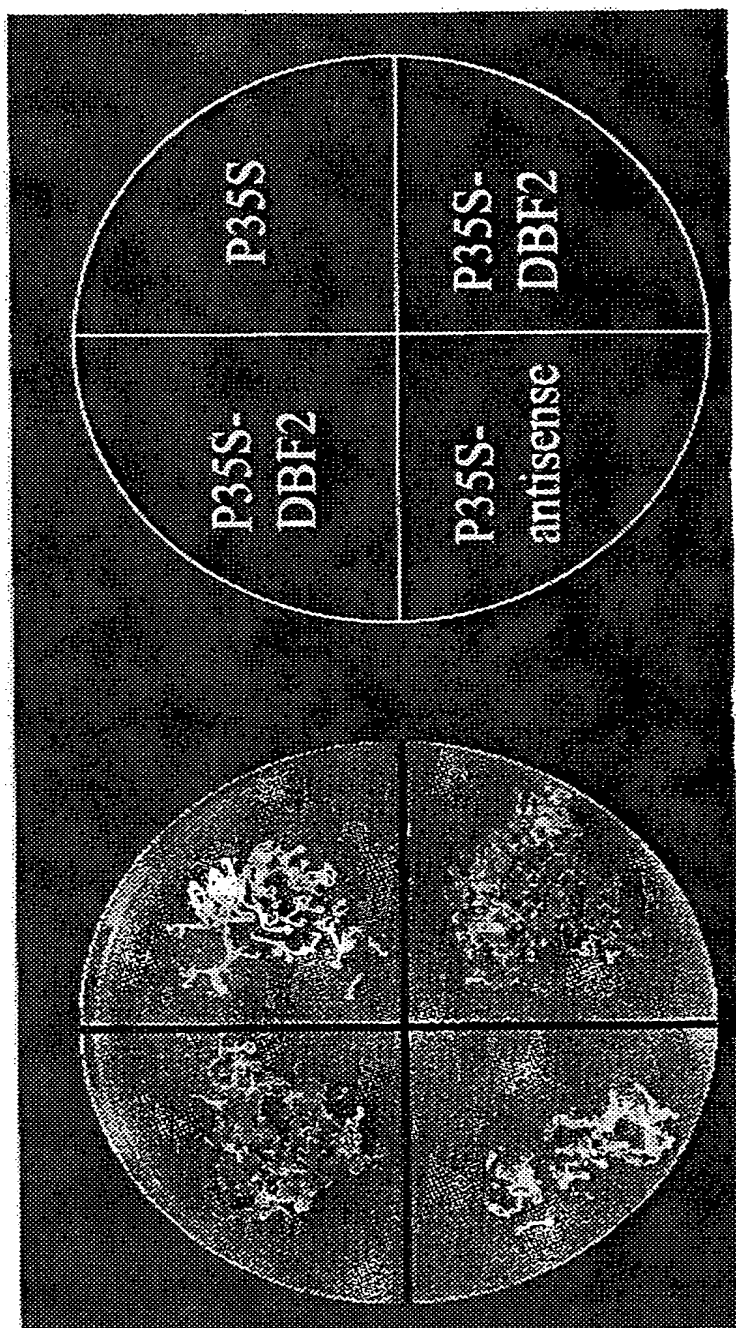


FIGURE 7

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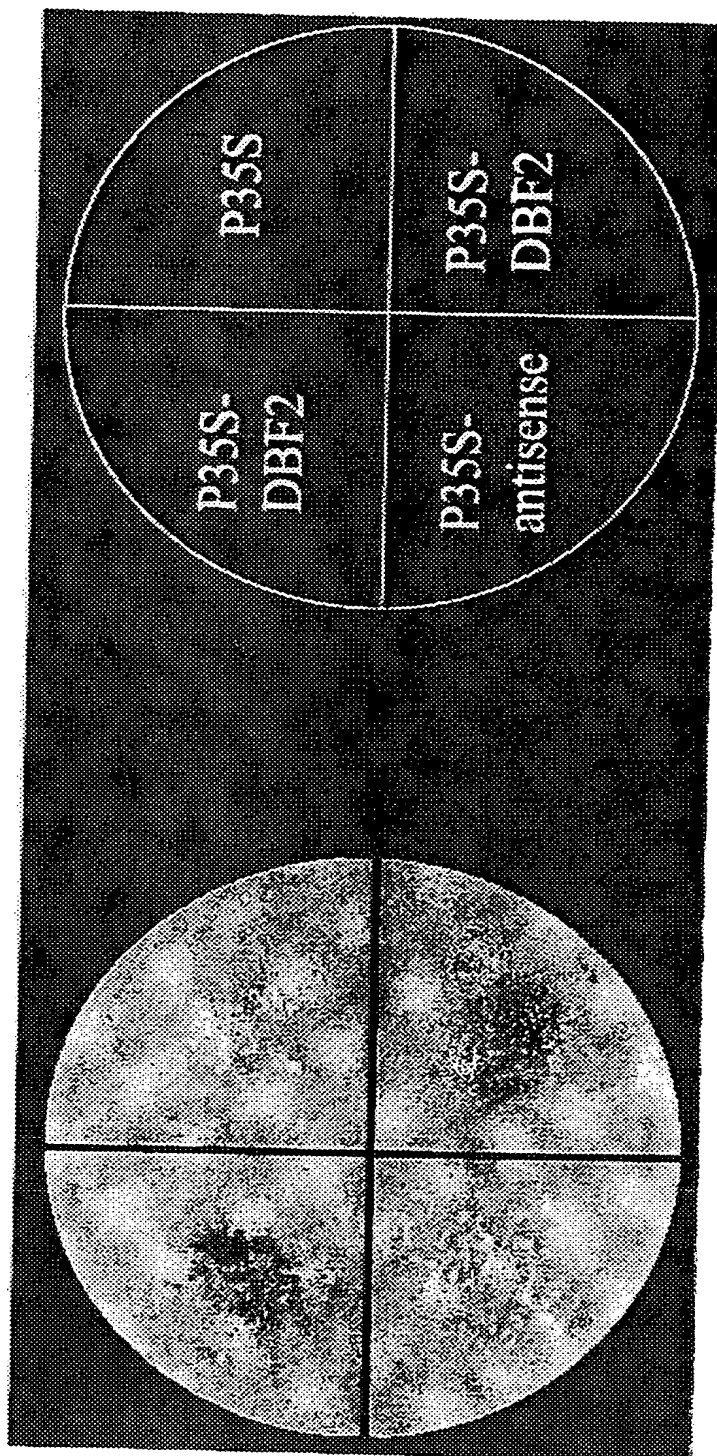


FIGURE 8

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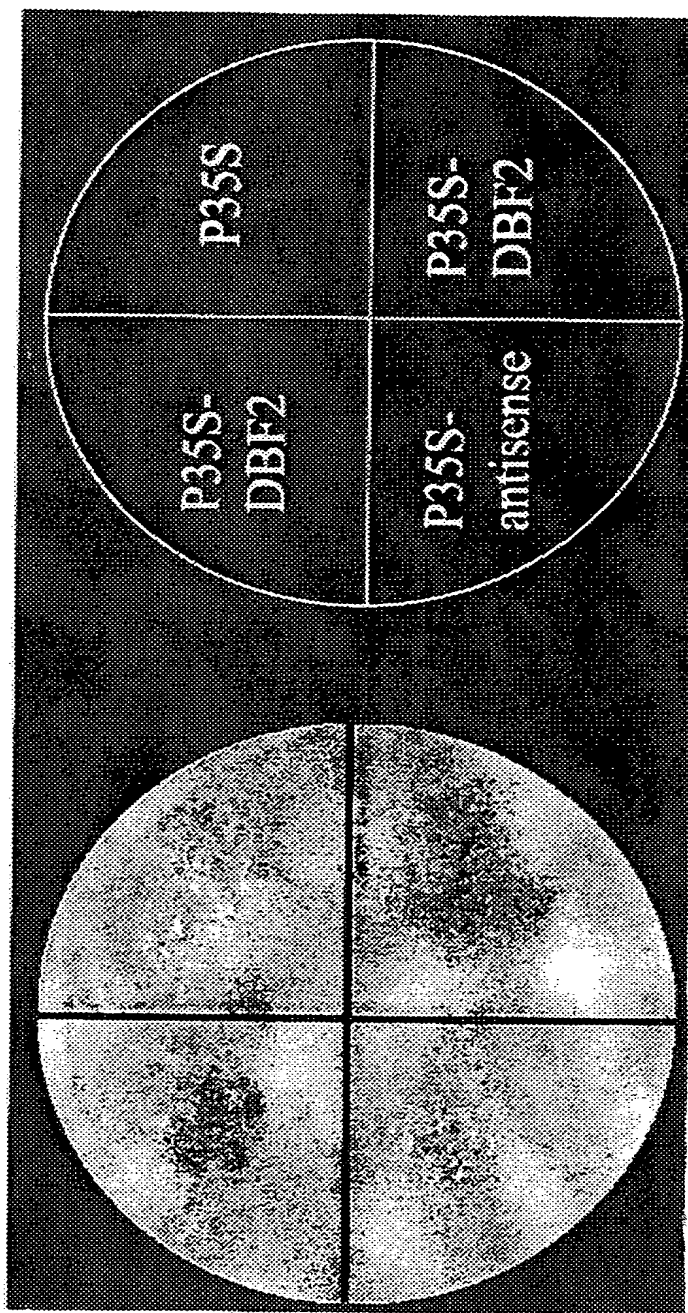


FIGURE 9

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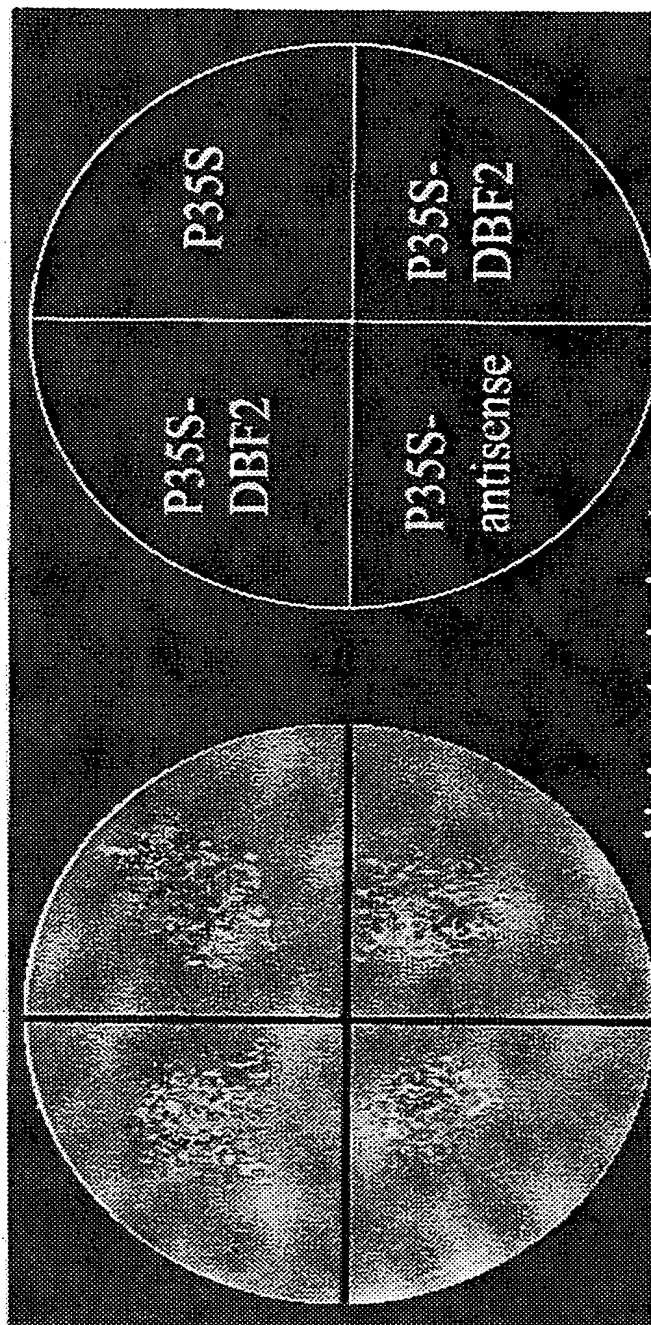


FIGURE 10

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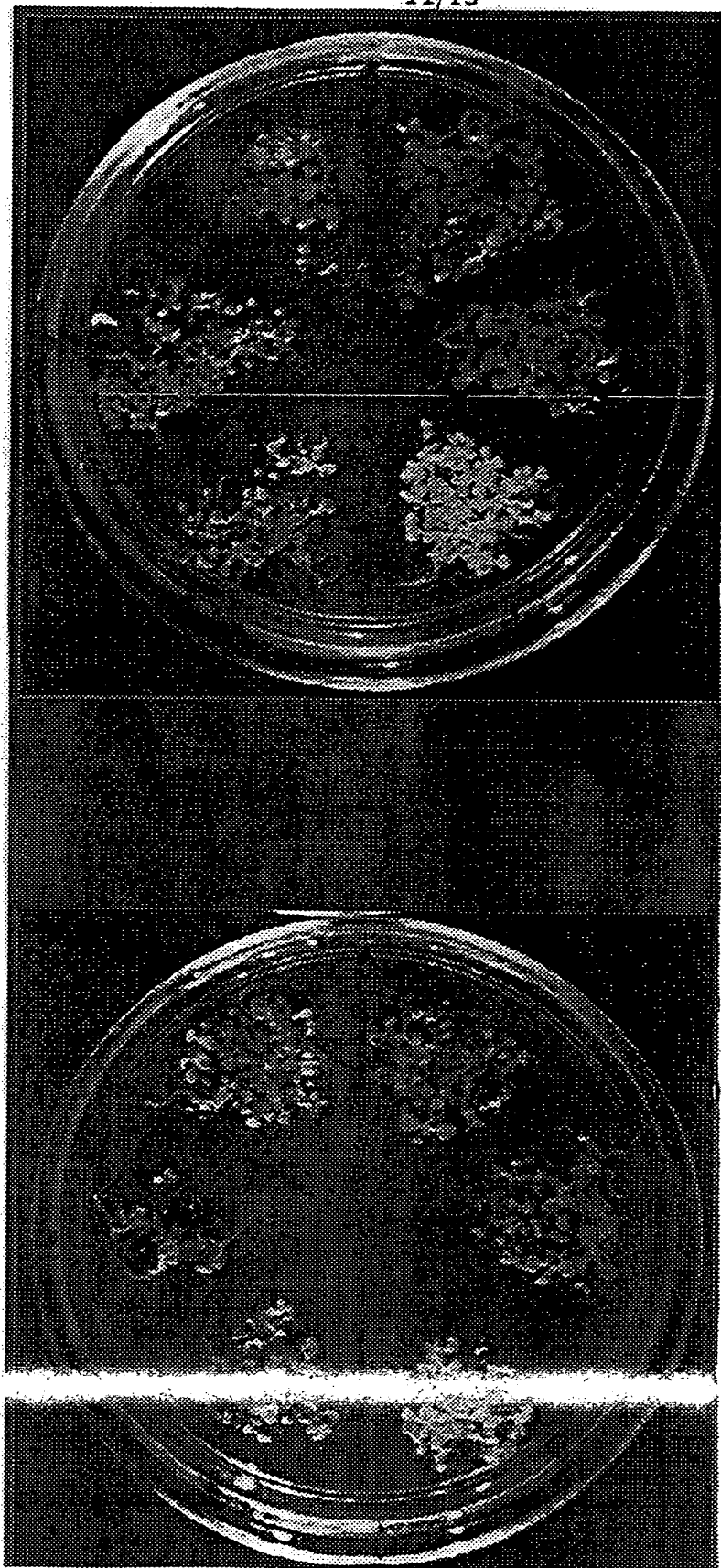


FIGURE 11

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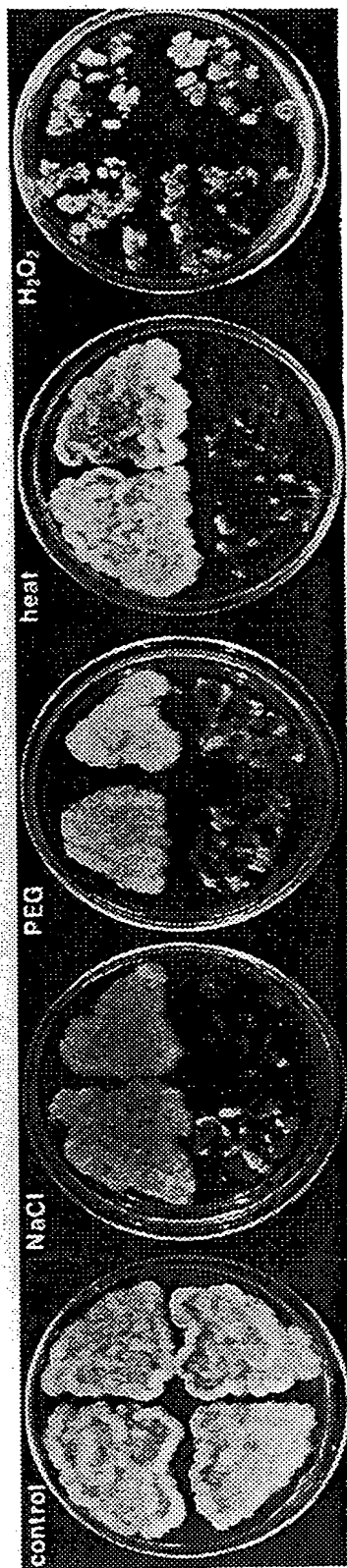


FIGURE 12A

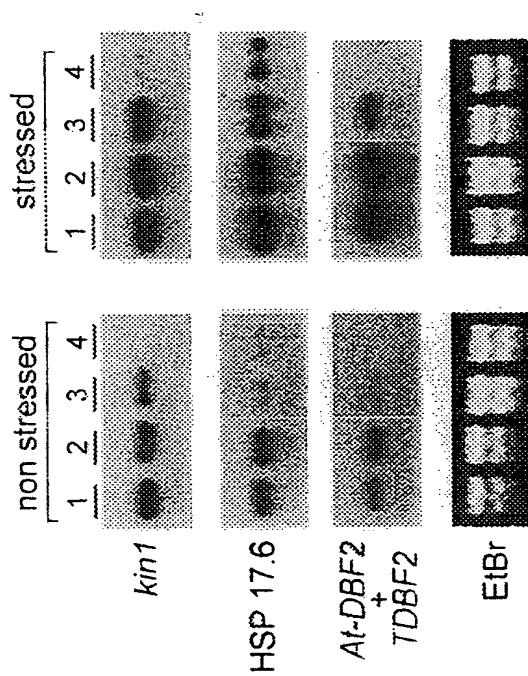


FIGURE 12c

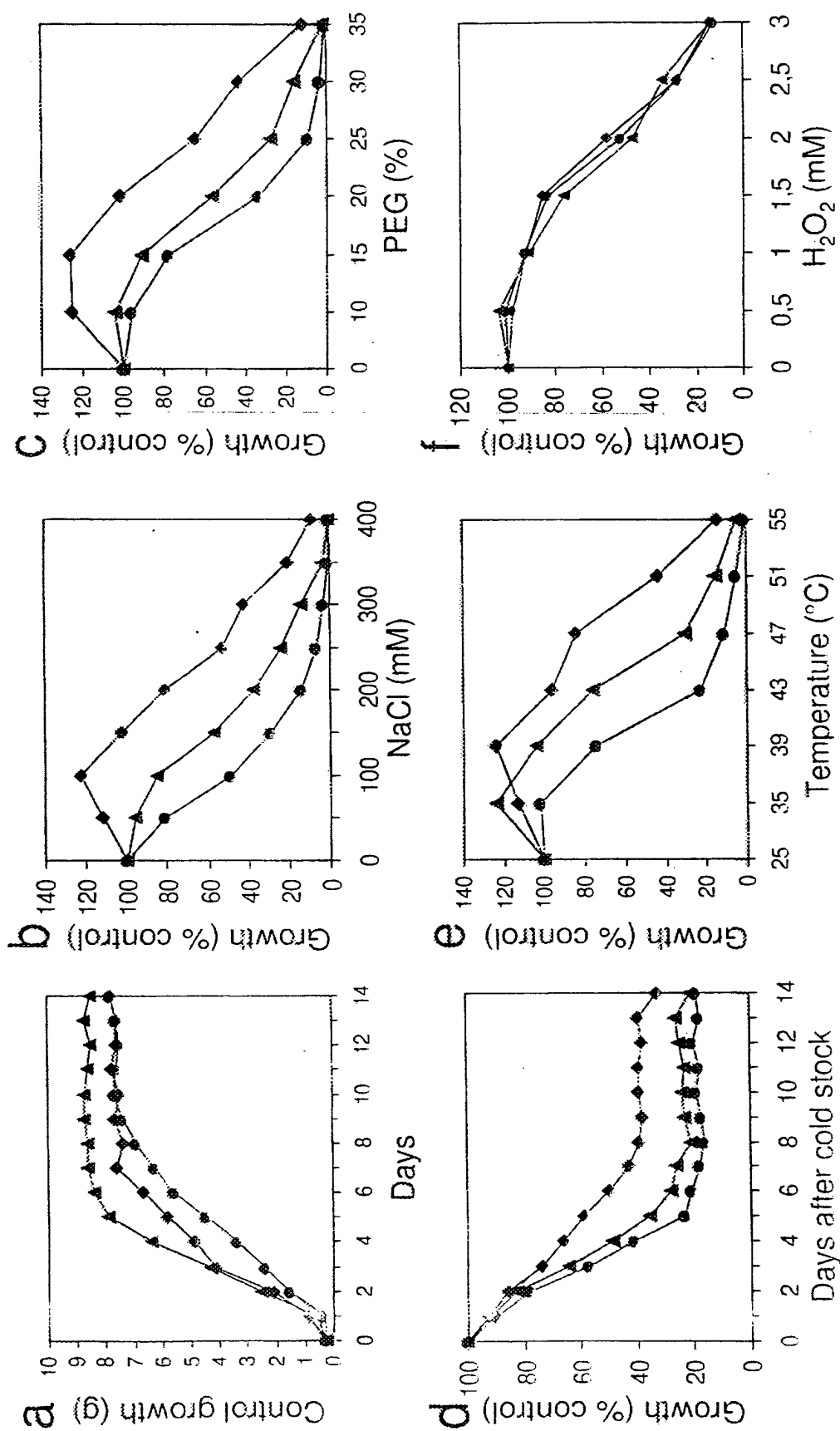


FIGURE 12B



FIGURE 13

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FIGURE 14

SEQUENCE LISTING

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 Ser Trp Lys Gln Thr Leu Asn Arg Ala Arg His Glu Asp Gly Arg Ala
 385 390 395 400
 Ala Phe Tyr Asn Arg Thr Trp Asp Leu Ile Thr Arg His Arg Ala Asp
 405 410 415
 Leu Ser Thr Arg Thr Arg Ser Phe Glu His Glu Val Lys Met Ser Tyr
 420 425 430
 Phe Ala Asp Ile Leu Phe Lys Ala Leu Arg Ser Ile Ile Pro Pro Phe
 435 440 445
 Thr Pro Gln Leu Asp Ser Glu Thr Asp Ala Gly Tyr Phe Asp Asp Phe
 450 455 460
 Trp Asn Glu Ala Asp Ile Ala Lys Tyr Ala Asp Val Phe Asn Ser Gln
 465 470 475 480
 Cys Cys Arg Thr Ala Leu Val Asp Asp Ser Ala Val Ser Ser Lys Leu
 485 490 495
 Val Gly Phe Thr Phe Arg His Arg Asn Gly Lys Gln Gly Ser Ser Gly
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                               Met Asp Leu Glu Phe Gly Arg
                               1                               5

ttt cca ata ttt tca atc ctc gaa gac atg ctt gaa gcc cct gaa gaa 162
Phe Pro Ile Phe Ser Ile Leu Glu Asp Met Leu Glu Ala Pro Glu Glu
                               10                               15                               20

caa acc gag aag act cgt aac aac cct tca aga gct tac atg cga gac 210
Gln Thr Glu Lys Thr Arg Asn Asn Pro Ser Arg Ala Tyr Met Arg Asp
                               25                               30                               35

gca aag gca atg gct gct aca cca gct gac gtt atc gag cac ccg gat 258
Ala Lys Ala Met Ala Ala Thr Pro Ala Asp Val Ile Glu His Pro Asp
                               40                               45                               50                               55

gcg tac gtt ttc gcc gtg gac atg cct gga atc aaa gga gat gag att 306
Ala Tyr Val Phe Ala Val Asp Met Pro Gly Ile Lys Gly Asp Glu Ile
                               60                               65                               70

cag gtc cag ata gag aac gag aac gtg ctt gtg gtg agt ggc aaa aga 354
Gln Val Gln Ile Glu Asn Glu Asn Val Leu Val Val Ser Gly Lys Arg
                               75                               80                               85

cag agg gac aac aag gag aat gaa ggt gtg aag ttt gtg agg atg gag 402
Gln Arg Asp Asn Lys Glu Asn Glu Gly Val Lys Phe Val Arg Met Glu
                               90                               95                               100

agg agg atg ggg aag ttt atg agg aag ttt cag tta cct gat aat gca 450
Arg Arg Met Gly Lys Phe Met Arg Lys Phe Gln Leu Pro Asp Asn Ala
                               105                               110                               115

gat ttg gag aag atc tct gcg gct tgt aat gac ggt gtg ttg aaa gtg 498
Asp Leu Glu Lys Ile Ser Ala Ala Cys Asn Asp Gly Val Leu Lys Val
                               120                               125                               130                               135

act att ccg aaa ctt cct cct cct gag cca aag aaa cca aag act ata 546
Thr Ile Pro Lys Leu Pro Pro Pro Glu Pro Lys Lys Pro Lys Thr Ile
                               140                               145                               150

caa gtt caa gtc gct tga gtttgtttgt gatccgtgtt tttgtgtttt 594
Gln Val Gln Val Ala
                               155

aatgaatgta atcgataagc aactacctct tgggtgttcgt tgtaaaatga aataaaaaata 654

gttttctctg ttcataaaaa aaaaaaaaaa aaaactcgag c 695
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 35 40 45
 Asp Val Ile Glu His Pro Asp Ala Tyr Val Phe Ala Val Asp Met Pro
 50 55 60
 Gly Ile Lys Gly Asp Glu Ile Gln Val Gln Ile Glu Asn Glu Asn Val
 65 70 75 80
 Leu Val Val Ser Gly Lys Arg Gln Arg Asp Asn Lys Glu Asn Glu Gly
 85 90 95
 Val Lys Phe Val Arg Met Glu Arg Arg Met Gly Lys Phe Met Arg Lys
 100 105 110
 Phe Gln Leu Pro Asp Asn Ala Asp Leu Glu Lys Ile Ser Ala Ala Cys
 115 120 125
 Asn Asp Gly Val Leu Lys Val Thr Ile Pro Lys Leu Pro Pro Pro Glu
 130 135 140
 Pro Lys Lys Pro Lys Thr Ile Gln Val Gln Val Ala
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 ttccaatcat cc atg agt ccg gac aat aaa ctg ctt ccg aag cgg atc atc 171
 Met Ser Pro Asp Asn Lys Leu Leu Pro Lys Arg Ile Ile
 1 5 10

ctt gta cgg cac ggt gaa tcg gaa ggg aat ctc gac acg gcg gcg tat	219
Leu Val Arg His Gly Glu Ser Glu Gly Asn Leu Asp Thr Ala Ala Tyr	
15 20 25	
aca acg acg ccg gat cat aag atc cag tta acg gat tcc ggt ttg ctt	267
Thr Thr Thr Pro Asp His Lys Ile Gln Leu Thr Asp Ser Gly Leu Leu	
30 35 40 45	
cag gcg cag gaa gcc gga gct cgt ctc cac gct ttg atc tct tct aat	315
Gln Ala Gln Glu Ala Gly Ala Arg Leu His Ala Leu Ile Ser Ser Asn	
50 55 60	
cct tct tca ccg gag tgg cgt gtg tac ttc tac gtt tcg ccg tac gat	363
Pro Ser Ser Pro Glu Trp Arg Val Tyr Phe Tyr Val Ser Pro Tyr Asp	
65 70 75	
cgg act cga tct acg ctc cgg gag atc gga cgg tcg ttc tcg cgt cgc	411
Arg Thr Arg Ser Thr Leu Arg Glu Ile Gly Arg Ser Phe Ser Arg Arg	
80 85 90	
cgt gtg att ggt gtt cgc gaa gaa tgt cgg att agg gaa cag gat ttt	459
Arg Val Ile Gly Val Arg Glu Glu Cys Arg Ile Arg Glu Gln Asp Phe	
95 100 105	
ggg aat ttt cag gtt aaa gag cga atg aga gca acg aaa aag gtc aga	507
Gly Asn Phe Gln Val Lys Glu Arg Met Arg Ala Thr Lys Lys Val Arg	
110 115 120 125	
gag aga ttt ggc cgc ttt ttt tac cgg ttc ccg gag gga gaa tcc gcc	555
Glu Arg Phe Gly Arg Phe Phe Tyr Arg Phe Pro Glu Gly Glu Ser Ala	
130 135 140	
gcc gat gtc ttc gat cgc gtc tcc agt ttt ctc gag tct cta tgg aga	603
Ala Asp Val Phe Asp Arg Val Ser Ser Phe Leu Glu Ser Leu Trp Arg	
145 150 155	
gac att gac atg aac aga ctg cac atc aac ccg tct cat gag cta aac	651
Asp Ile Asp Met Asn Arg Leu His Ile Asn Pro Ser His Glu Leu Asn	
160 165 170	
ttt gtg att gtc tca cat ggc tta aca tcg cgt gtg ttt ctg atg aaa	699
Phe Val Ile Val Ser His Gly Leu Thr Ser Arg Val Phe Leu Met Lys	
175 180 185	
tgg ttt aag tgg tca gtg gaa cag ttc gag gga cta aac aat cca ggg	747
Trp Phe Lys Trp Ser Val Glu Gln Phe Glu Gly Leu Asn Asn Pro Gly	
190 195 200 205	
aac agt gag atc aga gtg atg gaa tta gga caa ggc ggt gat tac agc	795
Asn Ser Glu Ile Arg Val Met Glu Leu Gly Gln Gly Gly Asp Tyr Ser	
210 215 220	
ttg gcg att cat cac aca gag gaa gag tta gcc aca tgg gga ctg tca	843
Leu Ala Ile His His Thr Glu Glu Glu Leu Ala Thr Trp Gly Leu Ser	
225 230 235	
cca gag atg att gca gat caa aag tgg ccg gct aac gcg cat aaa ggc	891

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Pro Glu Met Ile Ala Asp Gln Lys Trp Arg Ala Asn Ala His Lys Gly
      240                245                250

gaa tgg aaa gaa gat tgt aag tgg tat ttt ggt gat ttc ttc gac cat 939
Glu Trp Lys Glu Asp Cys Lys Trp Tyr Phe Gly Asp Phe Phe Asp His
      255                260                265

atg gca gat tcc gat aaa gag tgc gag act gag gcc act gaa gat aga 987
Met Ala Asp Ser Asp Lys Glu Cys Glu Thr Glu Ala Thr Glu Asp Arg
      270                275                280                285

gaa gaa gaa gaa gaa gaa gag ggg aaa agg gta aat ctg cta acg agt 1035
Glu Glu Glu Glu Glu Glu Glu Gly Lys Arg Val Asn Leu Leu Thr Ser
      290                295                300

tca gaa tat agc aat gag cca gag tta tac aat gga caa tgc tgc tga 1083
Ser Glu Tyr Ser Asn Glu Pro Glu Leu Tyr Asn Gly Gln Cys Cys
      305                310                315

tactattttta cagaacaaaa gcatacatga gaagaaacgt ttaactaaag aattcagaag 1143

atttgattttt gataaaaaact tgtaccaatt tactgattaa gcttttctggt gtcttagttt 1203

gtagctttttg gtttgtggaa aagtgttgta cacatcgtta taacaccagg aaacattaca 1263

ggaaatttga aagattcatt ttattgtgac aaaaaaaaaa aaaaaaaaaa 1311

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Pro Asp His Lys Ile Gln Leu Thr Asp Ser Gly Leu Leu Gln Ala Gln
      35                40                45

Glu Ala Gly Ala Arg Leu His Ala Leu Ile Ser Ser Asn Pro Ser Ser
      50                55                60

Pro Glu Trp Arg Val Tyr Phe Tyr Val Ser Pro Tyr Asp Arg Thr Arg
      65                70                75                80

Ser Thr Leu Arg Glu Ile Gly Arg Ser Phe Ser Arg Arg Arg Val Ile
      85                90                95

Gly Val Arg Glu Glu Cys Arg Ile Arg Glu Gln Asp Phe Gly Asn Phe
      100                105                110

Gln Val Lys Glu Arg Met Arg Ala Thr Lys Lys Val Arg Glu Arg Phe
      115                120                125

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Gly Arg Phe Phe Tyr Arg Phe Pro Glu Gly Glu Ser Ala Ala Asp Val
 130 135 140
 Phe Asp Arg Val Ser Ser Phe Leu Glu Ser Leu Trp Arg Asp Ile Asp
 145 150 155 160
 Met Asn Arg Leu His Ile Asn Pro Ser His Glu Leu Asn Phe Val Ile
 165 170 175
 Val Ser His Gly Leu Thr Ser Arg Val Phe Leu Met Lys Trp Phe Lys
 180 185 190
 Trp Ser Val Glu Gln Phe Glu Gly Leu Asn Asn Pro Gly Asn Ser Glu
 195 200 205
 Ile Arg Val Met Glu Leu Gly Gln Gly Gly Asp Tyr Ser Leu Ala Ile
 210 215 220
 His His Thr Glu Glu Glu Leu Ala Thr Trp Gly Leu Ser Pro Glu Met
 225 230 235 240
 Ile Ala Asp Gln Lys Trp Arg Ala Asn Ala His Lys Gly Glu Trp Lys
 245 250 255
 Glu Asp Cys Lys Trp Tyr Phe Gly Asp Phe Phe Asp His Met Ala Asp
 260 265 270
 Ser Asp Lys Glu Cys Glu Thr Glu Ala Thr Glu Asp Arg Glu Glu Glu
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 Glu Glu Glu Glu Gly Lys Arg Val Asn Leu Leu Thr Ser Ser Glu Tyr
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 Val Ala Ile Ile Thr Gly Gly Ala Arg Gly Ile Gly Ala Ala Thr Ala
 15 20 25

aga ttg ttc aca gag aat ggc gcg tat gtg ata gtc gcg gat atc ctt	147
Arg Leu Phe Thr Glu Asn Gly Ala Tyr Val Ile Val Ala Asp Ile Leu	
30 35 40	
gat aat gaa ggc atc ctt gtg gcg gaa tcg atc ggt ggg tgt tac gtt	195
Asp Asn Glu Gly Ile Leu Val Ala Glu Ser Ile Gly Gly Cys Tyr Val	
45 50 55	
cat tgt gac gta tcg aag gag gct gat gtt gag gcg gca gtg gag cta	243
His Cys Asp Val Ser Lys Glu Ala Asp Val Glu Ala Ala Val Glu Leu	
60 65 70 75	
gca atg aga cgt aaa ggt aga cta gat gtg atg ttc aac aat gcc ggg	291
Ala Met Arg Arg Lys Gly Arg Leu Asp Val Met Phe Asn Asn Ala Gly	
80 85 90	
atg tcg ctt aac gaa ggt agt atc atg ggg atg gac gtg gac atg gtt	339
Met Ser Leu Asn Glu Gly Ser Ile Met Gly Met Asp Val Asp Met Val	
95 100 105	
aac aaa ctt gtc tcg gtt aat gtc aat ggt gtt ttg cat ggt atc aaa	387
Asn Lys Leu Val Ser Val Asn Val Asn Gly Val Leu His Gly Ile Lys	
110 115 120	
cat gcc gct aag gcc atg atc aaa ggg gga cga gga ggc tcg ata ata	435
His Ala Ala Lys Ala Met Ile Lys Gly Gly Arg Gly Gly Ser Ile Ile	
125 130 135	
tgc aca tcg agc tca tca ggg cta atg gga gga ctt gga gga cat gcg	483
Cys Thr Ser Ser Ser Ser Gly Leu Met Gly Gly Leu Gly Gly His Ala	
140 145 150 155	
tat acg ctc tcc aaa gga ggc atc aac ggg gtg gtg agg aca acg gag	531
Tyr Thr Leu Ser Lys Gly Gly Ile Asn Gly Val Val Arg Thr Thr Glu	
160 165 170	
tgc gag ctt ggg tct cac ggc atc cgt gtg aat agc atc tct cct cat	579
Cys Glu Leu Gly Ser His Gly Ile Arg Val Asn Ser Ile Ser Pro His	
175 180 185	
gga gtt ccc act gac atc ttg gtt aat gcg tac cgt aag ttc ctt aac	627
Gly Val Pro Thr Asp Ile Leu Val Asn Ala Tyr Arg Lys Phe Leu Asn	
190 195 200	
aat gac aaa ctc aac gtc gct gag gtc acc gac att att gct gag aaa	675
Asn Asp Lys Leu Asn Val Ala Glu Val Thr Asp Ile Ile Ala Glu Lys	
205 210 215	
ggg agt ttg ctg acc gga aga gcc ggt act gtg gag gac gta gct caa	723
Gly Ser Leu Leu Thr Gly Arg Ala Gly Thr Val Glu Asp Val Ala Gln	
220 225 230 235	
gca gct ttg ttt ctt gca agc caa gaa tcg tcg ggg ttc att acc gga	771
Ala Ala Leu Phe Leu Ala Ser Gln Glu Ser Ser Gly Phe Ile Thr Gly	
240 245 250	
cat aac ttg gtt gtt gat ggt ggt tac aca tct gcc act agt act atg	819

His Asn Leu Val Val Asp Gly Gly Tyr Thr Ser Ala Thr Ser Thr Met
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 35 40 45

Leu Val Ala Glu Ser Ile Gly Gly Cys Tyr Val His Cys Asp Val Ser
 50 55 60

Lys Glu Ala Asp Val Glu Ala Ala Val Glu Leu Ala Met Arg Arg Lys
 65 70 75 80

Gly Arg Leu Asp Val Met Phe Asn Asn Ala Gly Met Ser Leu Asn Glu
 85 90 95

Gly Ser Ile Met Gly Met Asp Val Asp Met Val Asn Lys Leu Val Ser
 100 105 110

Val Asn Val Asn Gly Val Leu His Gly Ile Lys His Ala Ala Lys Ala
 115 120 125

Met Ile Lys Gly Gly Arg Gly Gly Ser Ile Ile Cys Thr Ser Ser Ser
 130 135 140

Ser Gly Leu Met Gly Gly Leu Gly Gly His Ala Tyr Thr Leu Ser Lys
 145 150 155 160

Gly Gly Ile Asn Gly Val Val Arg Thr Thr Glu Cys Glu Leu Gly Ser
 165 170 175

His Gly Ile Arg Val Asn Ser Ile Ser Pro His Gly Val Pro Thr Asp
 180 185 190

Ile Leu Val Asn Ala Tyr Arg Lys Phe Leu Asn Asn Asp Lys Leu Asn
 195 200 205

Val Ala Glu Val Thr Asp Ile Ile Ala Glu Lys Gly Ser Leu Leu Thr
 210 215 220

Gly Arg Ala Gly Thr Val Glu Asp Val Ala Gln Ala Ala Leu Phe Leu

225		230		235		240
Ala Ser Gln Glu Ser Ser Gly Phe Ile Thr Gly His Asn Leu Val Val						
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Asp Gly Gly Tyr Thr Ser Ala Thr Ser Thr Met Arg Phe Ile Tyr Asn						
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 atatatgctc gttttctaaa ctatttttta attggattga tgttcttaaa tcttaagggt 174
 caaaatactt tttatgctca aaaacttact taaattctgt gatcgcttga acctaagtgg 234
 atgatgtgga tttcctgttt tggctgctta tctttaagta aaacgtttta cccactgcgt 294
 gagaaagaca cgccacatgt ggtttttggt gtttttttcc ttagattaga agttattttg 354

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attaagtaat catcaacaaa atgattgac agatctatca atacaagtgt attttttttt 534
cacatacaaa aaaattatct caccgacgaa aaaaaaataa aaaattatta tgtagatcca 594
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gattgttgac caaattttct ctaggatttt tgttgataat cgatcgtata atgggtgattg 954

cag tat cgt cct tca agc gcg tac aac gcc cca ttc tac acc aca aac 1002
  Tyr Arg Pro Ser Ser Ala Tyr Asn Ala Pro Phe Tyr Thr Thr Asn
                10                15                20

ggg ggt gct cca gtc tcc aac aac atc tct tcc ctc acc atc gga gaa 1050
Gly Gly Ala Pro Val Ser Asn Asn Ile Ser Ser Leu Thr Ile Gly Glu
                25                30                35

aga g gtatcgtaac cctgaatttc aagagtctat caataagaat cggaacttgt 1104
Arg G

tggatttatg aaagagataa aactgagata tagagtctaa gctgagatct gttcgtgaag 1164

cgtgatgtga ttatttttaa catgtgttac ttcgtaatgg gcag gt ccg gtt ctt 1219
                ly Pro Val Leu
                        40

ctt gag gat tat cat ttg atc gag aag gtt gct aat ttc acc aga gag 1267
Leu Glu Asp Tyr His Leu Ile Glu Lys Val Ala Asn Phe Thr Arg Glu
                45                50                55

agg atc cct gag aga gtg gtt cat gct aga gga atc agt gct aag ggt 1315
Arg Ile Pro Glu Arg Val Val His Ala Arg Gly Ile Ser Ala Lys Gly
                60                65                70

ttc ttt gaa gtc acc cat gac att tca aac ctc act tgt gct gat ttt 1363
Phe Phe Glu Val Thr His Asp Ile Ser Asn Leu Thr Cys Ala Asp Phe
                75                80                85

ctc aga gcc cct ggt gtt caa act ccg gtt att gtc cgt ttc tca acg 1411
Leu Arg Ala Pro Gly Val Gln Thr Pro Val Ile Val Arg Phe Ser Thr
                90                95                100                105

gtt gtt cac gga cgt gcc agt cct gaa acc atg agg gat att cgt ggt 1459
Val Val His Gly Arg Ala Ser Pro Glu Thr Met Arg Asp Ile Arg Gly
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Phe Ala Val Lys Phe Tyr Thr Arg Glu
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gttatgatca g gga aac ttt gat ctt gtt ggg aac aac act ccg gtg ttc 1616
      Gly Asn Phe Asp Leu Val Gly Asn Asn Thr Pro Val Phe
      135                      140

ttc atc cgt gat ggg att cag ttc ccg gat gtt gtc cac gcg ttg aaa 1664
Phe Ile Arg Asp Gly Ile Gln Phe Pro Asp Val Val His Ala Leu Lys
      145                      150                      155

cct aac cga aaa aca aac atc caa gag tac tgg agg att ctg gac tac 1712
Pro Asn Arg Lys Thr Asn Ile Gln Glu Tyr Trp Arg Ile Leu Asp Tyr
160                      165                      170                      175

atg tcc cac ttg cct gag agt ttg ctc aca tgg tgc tgg atg ttt gat 1760
Met Ser His Leu Pro Glu Ser Leu Leu Thr Trp Cys Trp Met Phe Asp
      180                      185                      190

gat gtt ggt att cca caa gat tac agg cat atg gag ggt ttc ggt gtc 1808
Asp Val Gly Ile Pro Gln Asp Tyr Arg His Met Glu Gly Phe Gly Val
      195                      200                      205

cac acc tac act ctt att gcc aaa tct gga aaa gtt ctc ttt gtg aag 1856
His Thr Tyr Thr Leu Ile Ala Lys Ser Gly Lys Val Leu Phe Val Lys
      210                      215                      220

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Phe His Trp Lys Pro Thr Cys Gly Ile Lys Asn Leu Thr Asp Glu Glu
      225                      230                      235

gcc aag gtt gtt gga gga gcc aat cac agc cac gcc act aag gat ctc 1952
Ala Lys Val Val Gly Gly Ala Asn His Ser His Ala Thr Lys Asp Leu
240                      245                      250                      255

cac gat gcc att gca tct ggc aac tac ccc gag tgg aaa ctt ttc atc 2000
His Asp Ala Ile Ala Ser Gly Asn Tyr Pro Glu Trp Lys Leu Phe Ile
      260                      265                      270

cag acc atg gat cct gca gat gag gat aag ttt gac ttt gac cca ctt 2048
Gln Thr Met Asp Pro Ala Asp Glu Asp Lys Phe Asp Phe Asp Pro Leu
      275                      280                      285

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Asp Val Thr Lys Ile Trp Pro Glu Asp Ile Leu Pro Leu Gln Pro Val
      290                      295                      300

ggt cgc ttg gtt ctg aac agg acc att gac aac ttc ttc aat gaa act 2144
Gly Arg Leu Val Leu Asn Arg Thr Ile Asp Asn Phe Phe Asn Glu Thr
      305                      310                      315

gag cag ctt gcg ttc aac ccg ggt ctt gtg gtt cct gga atc tac tac 2192
Glu Gln Leu Ala Phe Asn Pro Gly Leu Val Val Pro Gly Ile Tyr Tyr

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320	325	330	335	
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Ser Asp Asp Lys Leu Leu Gln Cys Arg Ile Phe Ala Tyr Gly Asp Thr	340	345	350	
cag aga cat cgc ctt gga ccg aat tat ttg cag ctt cca gtc aat gct				2288
Gln Arg His Arg Leu Gly Pro Asn Tyr Leu Gln Leu Pro Val Asn Ala	355	360	365	
ccc aaa tgt gct cac cac aac aat cac cat gaa ggt ttt atg aac ttc				2336
Pro Lys Cys Ala His His Asn Asn His His Glu Gly Phe Met Asn Phe	370	375	380	
atg cac aga gat gag gag gtacgtctta gtacaccact tgagctacca				2384
Met His Arg Asp Glu Glu	385			
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			Ile	390
aat tac tac ccc tca aag ttt gat cct gtc cgc tgc gct gag aaa gtt				2490
Asn Tyr Tyr Pro Ser Lys Phe Asp Pro Val Arg Cys Ala Glu Lys Val	395	400	405	
ccc acc cct aca aac tcc tac act gga att cga aca aag gtccgattcc				2539
Pro Thr Pro Thr Asn Ser Tyr Thr Gly Ile Arg Thr Lys	410	415		
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		Cys Val Ile Lys Lys Glu Asn Asn	425	
420				
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Phe Lys Gln Ala Gly Asp Arg Tyr Arg Ser Trp Ala Pro Asp Arg Gln	430	435	440	
gac agg ttt gtt aag aga tgg gtg gag att cta tcg gag cca cgt ctc				2748
Asp Arg Phe Val Lys Arg Trp Val Glu Ile Leu Ser Glu Pro Arg Leu	445	450	455	
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Thr His Glu Ile Arg Gly Ile Trp Thr Ser Tyr Trp Leu Lys	460	465	470	
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		Ala Asp Arg Ser Leu Gly Gln	480	
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Lys Leu Ala Ser Arg Leu Asn Val Arg Pro Ser Ile	485	490		

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 Pro Asn Arg Lys Thr Asn Ile Gln Glu Tyr Trp Arg Ile Leu Asp Tyr
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 Met Ser His Leu Pro Glu Ser Leu Leu Thr Trp Cys Trp Met Phe Asp
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 His Thr Tyr Thr Leu Ile Ala Lys Ser Gly Lys Val Leu Phe Val Lys
 210 215 220
 Phe His Trp Lys Pro Thr Cys Gly Ile Lys Asn Leu Thr Asp Glu Glu

225	230	235	24
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Gln Thr Met Asp Pro Ala Asp Glu Asp Lys Phe Asp Phe Asp Pro Leu	275	280	285
Asp Val Thr Lys Ile Trp Pro Glu Asp Ile Leu Pro Leu Gln Pro Val	290	295	300
Gly Arg Leu Val Leu Asn Arg Thr Ile Asp Asn Phe Phe Asn Glu Thr	305	310	315
Glu Gln Leu Ala Phe Asn Pro Gly Leu Val Val Pro Gly Ile Tyr Tyr	325	330	335
Ser Asp Asp Lys Leu Leu Gln Cys Arg Ile Phe Ala Tyr Gly Asp Thr	340	345	350
Gln Arg His Arg Leu Gly Pro Asn Tyr Leu Gln Leu Pro Val Asn Ala	355	360	365
Pro Lys Cys Ala His His Asn Asn His His Glu Gly Phe Met Asn Phe	370	375	380
Met His Arg Asp Glu Glu Ile Asn Tyr Tyr Pro Ser Lys Phe Asp Pro	385	390	395
Val Arg Cys Ala Glu Lys Val Pro Thr Pro Thr Asn Ser Tyr Thr Gly	405	410	415
Ile Arg Thr Lys Cys Val Ile Lys Lys Glu Asn Asn Phe Lys Gln Ala	420	425	430
Gly Asp Arg Tyr Arg Ser Trp Ala Pro Asp Arg Gln Asp Arg Phe Val	435	440	445
Lys Arg Trp Val Glu Ile Leu Ser Glu Pro Arg Leu Thr His Glu Ile	450	455	460
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 35 40 45

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 Asp Lys Pro Asn Lys Thr Leu Ser Ile Ile Asp Ser Gly Ile Gly Met
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Phe	Thr	Val	Thr	Arg	Asp	Val	Asp	Gly	Glu	Pro	Leu	Gly	Arg	Gly	Thr	
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Lys	Ile	Ser	Leu	Phe	Leu	Lys	Asp	Asp	Gln							
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	Leu	Glu	Tyr	Leu	Glu	Glu	Arg	Arg	Leu	Lys	Asp	Leu	Val	Lys		
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Lys	Glu	Asn	Glu	Gly	Glu	Val	Glu	Glu	Val	Asp	Glu	Lys	Lys	Glu	Lys	
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Phe Lys Ala Ile Leu Phe Val Pro Lys Arg Ala Pro Phe Asp Leu Phe	
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Arg Gly Tyr Glu Val Leu Tyr Met Val Asp Ala Ile Asp Glu Tyr Ala	
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Leu Glu Glu Leu Ser Val Leu Thr Ser Leu Asp Pro Gly Asp Ser
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Asp Val Leu Asp Ala Ile Thr Lys His Leu Asp Ile Gly Ser Ser Tyr	
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Ser Gly Lys Arg Pro Leu Phe Gly Pro Asp Leu Pro Lys Thr Glu Glu	
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Ile Ser Asp Val Leu Asp Thr Phe Lys Val Ile Ser Glu Leu Pro Ser	
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Asp Cys Phe Gly Ala Tyr Ile Ile Ser Met Ala Thr Ser Pro Ser Asp	
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Val Leu Ala Val Glu Leu Leu Gln Arg Glu Cys His Val Lys Asn Pro	
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Leu Arg Val Val Pro Leu Phe Glu Lys Leu Ala Asp Leu Glu Ala Ala	
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Pro Ala Ala Val Ala Arg Leu Phe Ser Ile Asp Trp Tyr Lys Asn Arg	
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Ile Asn Gly Lys Gln Glu Val Met Ile Gly Tyr Ser Asp Ser Gly Lys	
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Asp Ala Gly Arg Leu Ser Ala Ala Trp Glu Leu Tyr Lys Ala Gln Glu	
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Cys Phe Arg Thr Leu Gln Arg Phe Thr Ala Ala Thr Leu Glu His Gly	
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Lys Leu Phe Gly Gly Thr Thr Pro Gly Thr Ile Thr Asn Lys Glu Trp
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Gly Ala Ala Thr Glu Glu Arg Leu Gln Ala Trp Pro Arg Val Ala Gly
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cct ccc gtc gtc atg aac cct atc agt cgc cag aat ttc atc gtc aag 244
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Ser Lys Thr Gly Gly Pro Asn Gly Ser Ile Arg Asn Glu Glu Glu His

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Thr His Gly Ala Asn Ser Gly Leu Lys Ile Ala Leu Asp Leu Cys Glu

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Gly Val Lys Ala Lys His Pro Lys Ile Thr Tyr Ala Asp Leu Tyr Gln

85 90 95

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100 105 110

Phe Val Pro Gly Arg Lys Asp Ser Asn Val Cys Pro Lys Glu Gly Arg

115 120 125

Leu Pro Asp Ala Lys Gln Gly Phe Gln His Leu Arg Asp Val Phe Tyr

130 135 140

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225                      230                      235                      240

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Ser	Glu	Leu	Arg	Pro	His	Ala	Gly	Gly	Asp	Tyr	Ser	Ile	Ala	Val	Val		
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caa	gcc	aat	tcc	agg	ctt	gaa	gat	cag	agt	cag	gtt	ttc	aca	tct	tct	196	
Gln	Ala	Asn	Ser	Arg	Leu	Glu	Asp	Gln	Ser	Gln	Val	Phe	Thr	Ser	Ser		
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Ser	Ala	Thr	Tyr	Val	Gly	Val	Tyr	Asp	Gly	His	Gly	Gly	Pro	Glu	Ala		
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tct	aga	ttc	gtt	aac	aga	cat	ctc	ttt	cct	tat	atg	cac	a	gtaagttata	294		
Ser	Arg	Phe	Val	Asn	Arg	His	Leu	Phe	Pro	Tyr	Met	His	L				
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Lys Gly Ile Arg Arg His Phe His Asp Asp Ile Ser Val Ile Val Val			
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Tyr Asp Gly His Gly Gly Pro Glu Ala Ser Arg Phe Val Asn Arg His
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Lys Gly Ile Arg Arg His Phe His Asp Asp Ile Ser Val Ile Val Val
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Tyr Leu Asp Gln Asn Lys Thr Ser Ser Ser Asn Ser Lys Leu Val Lys
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Lys Glu Val Ile Asp Val Asp Cys Ser Glu Lys Lys Asp Phe Val Ile															
10 15 20															
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Asp Trp Ser Ser Ala Met Asp Lys Glu Asp Glu Val Pro Glu Leu Glu															
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Ile Val Asn Thr Thr Lys Pro Thr Pro Pro Pro Pro Pro Thr Phe Phe															
40 45 50															
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Ser Asp Asp Gln Thr Asp Ser Pro Lys Leu Leu Thr Asp Arg Asp Leu															
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70 75 80 85															
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Leu Pro Asp Lys Gly Glu Lys Ile Arg Leu Lys Ile Ala Asp Leu Glu															
90 95 100															
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Glu Glu Lys Gln A															
105															

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46

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 Ala Gln Pro Ser Thr Val Ala Glu Gln Ala Ala Glu Leu Pro Glu Gly
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 Leu Ile Lys Leu Gln Leu Ala Ile Tyr Lys Leu Ile Val Asp Lys Thr
 305 310 315 320
 Cys Ser Leu Gln Glu Asp Ile Cys Tyr Pro Thr ArSeg Phe Leu Gln
 325 330 e 335
 Gln Gln Ile Ser Sr Ser Asn Gln Ile Ser Ala Asp Cys His Phe Phe
 340e 345 350
 Asn Thr Tyr Phe Tr Lys Lys Leu Ser Asp Ala Val Thr Tyr Lys Gly
 355y 360 365
 Asn Asp Lys Ap Ala Phe Phe Val Arg Phe Arg Arg Trp Trp Lys Gly
 370 375 380
 Ile Asp Leu Pe Arg Lys Ala Tyr Ile Phe Ile Pro Ile His Glu r
 385 390 395u
 Leu His Trp Ser Leu Val Ile Val Cys Ile Pro Asp Lys Lys Asp Glu
 400 405 410
 Ser Gly Leu Thr Ile Leu His Leu Asp Ser Leu Gly Leu His Ser Arg
 415 420 425
 Lys Ser Ile Val Glu Asn Val Lys Arg Phe Leu Lys Asp Glu Trp Asn
 430 435 440
 Tyr Leu Asn Gln Asp Asp Tyr Ser Leu Asp Leu Pro Ile Ser Glu Lys

445 450 455 460
 Val Trp Lys Asn Leu Pro Arg Arg Ile Ser Glu Ala Val Val Gln Val
 465 470 475
 Pro Gln Gln Lys Asn Asp Phe Asp Cys Gly Pro Phe Val Leu Phe Phe
 480 485 490
 Ile Lys Arg Phe Ile Glu Glu Ala Pro Gln Arg Leu Lys Arg Lys Asp
 495 500 505
 Leu Gly Met Phe Asp Lys Lys Trp Phe Arg Pro Asp Glu Ala Ser Ala
 510 515 520
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 Asp Gln Thr Glu

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 Gly Thr Arg Leu Arg Pro Leu Thr Leu Ser Phe Pro Lys Pro Leu Val
 15 20 25
 gat ttt gct aat aaa ccc atg atc ctt cat cag ata gag gct ctt aag 147
 Asp Phe Ala Asn Lys Pro Met Ile Leu His Gln Ile Glu Ala Leu Lys
 30 35 40
 gca gtt gga gtt gat gaa gtg gtt ttg gcc atc aat tat cag cca gag 195
 Ala Val Gly Val Asp Glu Val Val Leu Ala Ile Asn Tyr Gln Pro Glu
 45 50 55
 gtg atg ctg aac ttc ttg aag gac ttt gag acc aag ctg gaa atc aaa 243
 Val Met Leu Asn Phe Leu Lys Asp Phe Glu Thr Lys Leu Glu Ile Lys
 60 65 70
 atc act tgc tca caa gag acc gag cca cta ggt acc gct ggt cct ctg 291
 Ile Thr Cys Ser Gln Glu Thr Glu Pro Leu Gly Thr Ala Gly Pro Leu
 75 80 85 90
 gct cta gcg aga gac aaa ttg ctt gat gga tct gga gag ccc ttc ttt 339
 Ala Leu Ala Arg Asp Lys Leu Leu Asp Gly Ser Gly Glu Pro Phe Phe

95										100					105					
gtt	ctt	aac	agt	gat	gtg	att	agt	gag	tac	cct	ctt	aaa	gaa	atg	ctt	387				
Val	Leu	Asn	Ser	Asp	Val	Ile	Ser	Glu	Tyr	Pro	Leu	Lys	Glu	Met	Leu					
			110						115			120								
gag	ttt	cac	aaa	tct	cac	ggt	ggg	gaa	gcc	tcc	ata	atg	gta	aca	aag	435				
Glu	Phe	His	Lys	Ser	His	Gly	Gly	Glu	Ala	Ser	Ile	Met	Val	Thr	Lys					
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gtg	gat	gaa	ccg	tcg	aaa	tat	gga	gtg	ggt	ggt	atg	gaa	gaa	agc	act	483				
Val	Asp	Glu	Pro	Ser	Lys	Tyr	Gly	Val	Val	Val	Met	Glu	Glu	Ser	Thr					
			140						145			150								
gga	aga	gtg	gag	aag	ttt	gtg	gaa	aag	cca	aaa	ctg	tat	gta	ggt	aac	531				
Gly	Arg	Val	Glu	Lys	Phe	Val	Glu	Lys	Pro	Lys	Leu	Tyr	Val	Gly	Asn					
			155						160			165			170					
aag	atc	aac	gct	ggg	att	tat	ctt	ctg	aac	cca	tct	ggt	ctt	gat	aag	579				
Lys	Ile	Asn	Ala	Gly	Ile	Tyr	Leu	Leu	Asn	Pro	Ser	Val	Leu	Asp	Lys					
			175						180			185								
att	gag	cta	aga	ccg	act	tca	atc	gaa	aaa	gag	act	ttc	cct	aag	att	627				
Ile	Glu	Leu	Arg	Pro	Thr	Ser	Ile	Glu	Lys	Glu	Thr	Phe	Pro	Lys	Ile					
			190						195			200								
gca	gca	gcg	caa	ggg	ctc	tat	gct	atg	gtg	cta	cca	ggg	ttt	tgg	atg	675				
Ala	Ala	Ala	Gln	Gly	Leu	Tyr	Ala	Met	Val	Leu	Pro	Gly	Phe	Trp	Met					
			205						210			215								
gac	att	ggg	caa	ccc	cgt	gac	tac	ata	acg	ggt	ttg	aga	ctc	tac	tta	723				
Asp	Ile	Gly	Gln	Pro	Arg	Asp	Tyr	Ile	Thr	Gly	Leu	Arg	Leu	Tyr	Leu					
			220						225			230								
gac	tcc	ctt	agg	aag	aaa	tct	cct	gcc	aaa	tta	acc	agt	ggg	cca	cac	771				
Asp	Ser	Leu	Arg	Lys	Lys	Ser	Pro	Ala	Lys	Leu	Thr	Ser	Gly	Pro	His					
			235						240			245			250					
ata	gtt	ggg	aat	gtt	ctt	gtt	gac	gaa	acc	gct	aca	att	ggg	gaa	gga	819				
Ile	Val	Gly	Asn	Val	Leu	Val	Asp	Glu	Thr	Ala	Thr	Ile	Gly	Glu	Gly					
			255						260			265								
tgt	ttg	att	gga	cca	gac	gtt	gcc	att	ggt	cca	ggc	tgc	att	gtt	gag	867				
Cys	Leu	Ile	Gly	Pro	Asp	Val	Ala	Ile	Gly	Pro	Gly	Cys	Ile	Val	Glu					
			270						275			280								
tca	gga	gtc	aga	ctc	tcc	cga	tgc	acg	gtc	atg	cgt	gga	gtc	cgc	atc	915				
Ser	Gly	Val	Arg	Leu	Ser	Arg	Cys	Thr	Val	Met	Arg	Gly	Val	Arg	Ile					
			285						290			295								
aag	aag	cat	gcg	tgt	atc	tcg	agc	agt	atc	atc	ggg	tgg	cac	tca	acg	963				
Lys	Lys	His	Ala	Cys	Ile	Ser	Ser	Ser	Ile	Ile	Gly	Trp	His	Ser	Thr					
			300						305			310								
gtt	ggt	caa	tgg	gcc	agg	atc	gag	aac	atg	acg	atc	ctc	ggt	gag	gat	1011				
Val	Gly	Gln	Trp	Ala	Arg	Ile	Glu	Asn	Met	Thr	Ile	Leu	Gly	Glu	Asp					
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gtt cat gtg agc gat gag atc tat agc aat gga gga gtt gtt ttg cca 1059
 Val His Val Ser Asp Glu Ile Tyr Ser Asn Gly Gly Val Val Leu Pro
 335 340 345

cac aag gag atc aaa tca aac atc ttg aag cca gag ata gtg atg tga 1107
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aa 1109

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 35 40 45

Val Val Leu Ala Ile Asn Tyr Gln Pro Glu Val Met Leu Asn Phe Leu
 50 55 60

Lys Asp Phe Glu Thr Lys Leu Glu Ile Lys Ile Thr Cys Ser Gln Glu
 65 70 75 80

Thr Glu Pro Leu Gly Thr Ala Gly Pro Leu Ala Leu Ala Arg Asp Lys
 85 90 95

Leu Leu Asp Gly Ser Gly Glu Pro Phe Phe Val Leu Asn Ser Asp Val
 100 105 110

Ile Ser Glu Tyr Pro Leu Lys Glu Met Leu Glu Phe His Lys Ser His
 115 120 125

Gly Gly Glu Ala Ser Ile Met Val Thr Lys Val Asp Glu Pro Ser Lys
 130 135 140

Tyr Gly Val Val Val Met Glu Glu Ser Thr Gly Arg Val Glu Lys Phe
 145 150 155 160

Val Glu Lys Pro Lys Leu Tyr Val Gly Asn Lys Ile Asn Ala Gly Ile
 165 170 175

Tyr Leu Leu Asn Pro Ser Val Leu Asp Lys Ile Glu Leu Arg Pro Thr
 180 185 190

Ser Ile Glu Lys Glu Thr Phe Pro Lys Ile Ala Ala Ala Gln Gly Leu
 195 200 205

Tyr Ala Met Val Leu Pro Gly Phe Trp Met Asp Ile Gly Gln Pro Arg
 210 215 220
 Asp Tyr Ile Thr Gly Leu Arg Leu Tyr Leu Asp Ser Leu Arg Lys Lys
 225 230 235 240
 Ser Pro Ala Lys Leu Thr Ser Gly Pro His Ile Val Gly Asn Val Leu
 245 250 255
 Val Asp Glu Thr Ala Thr Ile Gly Glu Gly Cys Leu Ile Gly Pro Asp
 260 265 270
 Val Ala Ile Gly Pro Gly Cys Ile Val Glu Ser Gly Val Arg Leu Ser
 275 280 285
 Arg Cys Thr Val Met Arg Gly Val Arg Ile Lys Lys His Ala Cys Ile
 290 295 300
 Ser Ser Ser Ile Ile Gly Trp His Ser Thr Val Gly Gln Trp Ala Arg
 305 310 315 320
 Ile Glu Asn Met Thr Ile Leu Gly Glu Asp Val His Val Ser Asp Glu
 325 330 335
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 cct tat cga acc aac tct tct ttc ggc tca aag tca tcg ctt ctc ttt 98
 Pro Tyr Arg Thr Asn Ser Ser Phe Gly Ser Lys Ser Ser Leu Leu Phe
 15 20 25 30
 cgg tct cca tcc tcc tcc tcc tca gtc tct atg acg aca acg cgt gga 146
 Arg Ser Pro Ser Ser Ser Ser Ser Val Ser Met Thr Thr Thr Arg Gly
 35 40 45
 aac gtg gct gtg gcg gct gct gct aca tcc act gag gcg cta aga aaa 194
 Asn Val Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys
 50 55 60

gga ata gcg gag ttc tac aat gaa act tcg ggt ttg tgg gaa gag att	242
Gly Ile Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile	
65 70 75	
tgg gga gat cat atg cat cat ggc ttt tat gac cct gat tct tct gtt	290
Trp Gly Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val	
80 85 90	
caa ctt tct gat tct ggt cac aag gaa gct cag atc cgt atg att gaa	338
Gln Leu Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu	
95 100 105 110	
gag tct ctc cgt ttc gcc ggt gtt act gat gaa gag gag gag aaa aag	386
Glu Ser Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys	
115 120 125	
ata aag aaa gta gtg gat gtt ggg tgt ggg att gga gga agc tca aga	434
Ile Lys Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg	
130 135 140	
tat ctt gcc tct aaa ttt gga gct gaa tgc att ggc att act ctc agc	482
Tyr Leu Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser	
145 150 155	
cct gtt cag gcc aag aga gcc aat gat ctc gcg gct gct caa tca ctc	530
Pro Val Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu	
160 165 170	
tct cat aag gct tcc ttc caa gtt gcg gat gcg ttg gat cag cca ttc	578
Ser His Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe	
175 180 185 190	
gaa gat gga aaa ttc gat cta gtg tgg tcg atg gag agt ggt gag cat	626
Glu Asp Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His	
195 200 205	
atg cct gac aag gcc aag ttt gta aaa gag ttg gta cgt gtg gcg gct	674
Met Pro Asp Lys Ala Lys Phe Val Lys Glu Leu Val Arg Val Ala Ala	
210 215 220	
cca gga ggt agg ata ata ata gtg aca tgg tgc cat aga aat cta tct	722
Pro Gly Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser	
225 230 235	
gcg ggg gag gaa gct ttg cag ccg tgg gag caa aac atc ttg gac aaa	770
Ala Gly Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys	
240 245 250	
atc tgt aag acg ttc tat ctc ccg gct tgg tgc tcc acc gat gat tat	818
Ile Cys Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr	
255 260 265 270	
gtc aac ttg ctt caa tcc cat tct ctc cag gat att aag tgt gcg gat	866
Val Asn Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp	
275 280 285	

tgg tca gag aac gta gct cct ttc tgg cct gcg gtt ata cgg act gca 914
 Trp Ser Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala
 290 295 300
 tta aca tgg aag ggc ctt gtg tct ctg ctt cgt agt ggt atg aaa agt 962
 Leu Thr Trp Lys Gly Leu Val Ser Leu Leu Arg Ser Gly Met Lys Ser
 305 310 315
 att aaa gga gca ttg aca atg cca ttg atg att gaa ggt tac aag aaa 1010
 Ile Lys Gly Ala Leu Thr Met Pro Leu Met Ile Glu Gly Tyr Lys Lys
 320 325 330
 ggt gtc att aag ttt ggt atc atc act tgc cag aag cca ctc taa 1055
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 335 340 345
 gtctaaagct atacta 1071

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 <213> Arabidopsis thaliana

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 35 40 45
 Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys Gly Ile
 50 55 60
 Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile Trp Gly
 65 70 75 80
 Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val Gln Leu
 85 90 95
 Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu Glu Ser
 100 105 110
 Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys Ile Lys
 115 120 125
 Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Tyr Leu
 130 135 140
 Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser Pro Val
 145 150 155 160
 Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu Ser His
 165 170 175

Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe Glu Asp
180 185 190

Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His Met Pro
195 200 205

Asp Lys Ala Lys Phe Val Lys Glu Leu Val Arg Val Ala Ala Pro Gly
210 215 220

Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser Ala Gly
225 230 235 240

Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys Ile Cys
245 250 255

Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr Val Asn
260 265 270

Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp Trp Ser
275 280 285

Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala Leu Thr
290 295 300

Trp Lys Gly Leu Val Ser Leu Leu Arg Ser Gly Met Lys Ser Ile Lys
305 310 315 320

Gly Ala Leu Thr Met Pro Leu Met Ile Glu Gly Tyr Lys Lys Gly Val
325 330 335

Ile Lys Phe Gly Ile Ile Thr Cys Gln Lys Pro Leu
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ctc gag atc gac gat gac cag aaa cta cgt gcg ttt tac gac aag aga 95
Leu Glu Ile Asp Asp Asp Gln Lys Leu Arg Ala Phe Tyr Asp Lys Arg
20 25 30

atc tct caa gaa gtc agt gga gat gct ttg ggc gag gag ttc aaa gga 143
Ile Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly
35 40 45

SS

tac gtt ttc aag atc aag ggt ggt tgc gat aag caa ggt ttc cca atg	191
Tyr Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met	
50 55 60	
aag cag gga gtt ttg act cca ggc cgt gtt cgc ctt ttg ctt cac cga	239
Lys Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg	
65 70 75	
gga act cct tgc ttc aga gga cat gga agg aga act ggt gag agg aga	287
Gly Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg	
80 85 90 95	
aga aag tct gtt cgt ggt tgc att gtg agc cct gat ctc tct gtt ctg	335
Arg Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu	
100 105 110	
aac ctt gtc att gtg aag aag ggt gag aac gat ctt cct ggg ctt acc	383
Asn Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr	
115 120 125	
gat cat gag agc aag atg aga gga cca aag aga gcc tcc aag atc cgt	431
Asp His Glu Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg	
130 135 140	
aaa ctg ttt aac ctc aag aag gaa gat gat gtc agg acc tat gtc aac	479
Lys Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn	
145 150 155	
act tac cgc cgc aag ttc aca aac aag aag ggc aag gaa gtt agc aaa	527
Thr Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys	
160 165 170 175	
gcc cct aag atc cag agg ctt gtg acc cca ttg act ctt cag agg aag	575
Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys	
180 185 190	
aga gct aga att gct gac aag aag aag aaa att gct aag gct aat tct	623
Arg Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser	
195 200 205	
gat gct gct gat tac cag aag ctt ctc gcc tcg agg ttg aag gaa cag	671
Asp Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln	
210 215 220	
cgt gac agg agg agt gag agt ttg gca aaa gag agg tcg aga ctc tct	719
Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Glu Arg Ser Arg Leu Ser	
225 230 235	
tct gct gct gcc aag ccc tct gtc aca gct taa aaaagcttga gattca	768
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<211> 249

<212> PRT

<213> Arabidopsis thaliana

<400> 28

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Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly Tyr
          35           40           45

Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met Lys
          50           55           60

Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg Gly
 65           70           75           80

Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg Arg
          85           90           95

Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu Asn
          100          105          110

Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr Asp
          115          120          125

His Glu Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg Lys
          130          135          140

Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn Thr
          145          150          155          160

Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys Ala
          165          170          175

Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys Arg
          180          185          190

Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser Asp
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Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln Arg
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 ctcttctctt ttctctgtca ctaattttca g act gag aaa gct ttt ctt aag 167
 Thr Glu Lys Ala Phe Leu Lys
 5 10

cag cct aag gtc ttc ctt ag gtaattttgc gattcgattt ctctctgttc 217
 Gln Pro Lys Val Phe Leu Se
 15

tctattgttt cattgtattt aagttccaag ttgtttatat tgttcattgt ttctgattta 277
 tcaag c tcg aag aaa tct gga aag gga aag aga cct gga aaa ggt gga 325
 r Ser Lys Lys Ser Gly Lys Gly Lys Arg Pro Gly Lys Gly Gly
 20 25 30

aac cgt ttc tgg aag aac att ggt ttg ggc ttc aag act cct cgt gaa 373
 Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg Glu
 35 40 45

gcc att gat g gtatgttttaa gcttttaact cggtataata gataaggaac 423
 Ala Ile Asp G
 50

tcttggattg tggtgttcat atagtcgata gatttcaaata gctattttgt cttgtagaat 483

cttaagcttt ggttttagtga gttctgattc ttcagcttta tctggatcta cattactgtt 543

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tcagtgatgc aaatgttatc agtagatttt gaattagtag gatgtcactg atttgaatat 603
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gttattgtgt atttgtgtgg aacag ga gct tac gtt gac aag aaa tgc ccc      714
                        ly Ala Tyr Val Asp Lys Lys Cys Pro
                        55                        60

ttc act gga act gtt tcc att aga ggt cgt atc tta gct ggt act tgc      762
Phe Thr Gly Thr Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys
                        65                        70                        75

cac agt gcg aaa atg cag agg acc att atc gtg cga agg gat tac ctt      810
His Ser Ala Lys Met Gln Arg Thr Ile Ile Val Arg Arg Asp Tyr Leu
                        80                        85                        90

cac ttt gtg aag aag tat cag ag gtaaattcat acattctcat acttctttcc      863
His Phe Val Lys Lys Tyr Gln Ar
                        95

atagagtctt acacattgat gtttaagaaa gtaatatcct tttgttctt ag g tat      919
                        g Tyr
                        100

gag aag agg cat tca aac att ccg gct cat gtc tca cca tgc ttc cgt      967
Glu Lys Arg His Ser Asn Ile Pro Ala His Val Ser Pro Cys Phe Arg
                        105                        110                        115

gtt aag gaa gga gac cat atc atc att ggc caa tgc ag gttatgatct      1015
Val Lys Glu Gly Asp His Ile Ile Ile Gly Gln Cys Ar
                        120                        125

gattcaaacc tacaaattgt ctccattgat tctgattatc gtgaatttgt tttgatcttt 1075
ttgtttgtta atgattgata atttcag g cca ttg tgc aag aca gtg agg ttc      1127
                        g Pro Leu Ser Lys Thr Val Arg Phe
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aat gtg ttg aag gtg ata cca gct ggg tct tct tct tca ttt gga aag      1175
Asn Val Leu Lys Val Ile Pro Ala Gly Ser Ser Ser Ser Phe Gly Lys
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 Glu Ala Ile Asp Gly Ala Tyr Val Asp Lys Lys Cys Pro Phe Thr Gly
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 Thr Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys His Ser Ala
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 Val Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Ile Ile Ile Gly
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 Gly Asn Trp Lys Ala Cys Pro Phe Ile Leu Gly Asn Glu Cys Cys Glu
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Asp Ala Tyr Trp Gly Arg Tyr Trp Thr Ile Ala Cys Phe Ser Gly Ile	
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Pro Thr Val Phe Met Gly Leu Ala Ile Ala Ser Phe Phe Phe Gly Thr	
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Val Tyr Ala Gln Met Ser Thr Met Phe Val Gln Gln Gly Arg Ala Met	
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Gln Ile Pro Gln Tyr Phe Ile Leu Gly Ala Ala Glu Val Phe Tyr Phe	
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Ile Gly Gln Leu Glu Phe Phe Tyr Asp Gln Ser Pro Asp Ala Met Arg	
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Tyr Phe Phe Trp Leu Leu Ala Gly Leu Ser Leu Val Asn Met Ala Val			
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 Ile Ala Gly Asn Leu Ile Thr Tyr Leu Thr Thr Lys Leu His Gln Gly
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 Cys Val Ser Ser Phe Gly Ala Asp Gln Phe Asp Asp Thr Asp Ser Arg
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 Glu Arg Val Arg Lys Ala Ser Phe Phe Asn Trp Phe Tyr Phe Ser Ile
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 Asn Arg Gly Trp Gly Leu Gly Phe Gly Ile Pro Thr Val Phe Met Gly
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 Gly Leu Ser Gly Phe Val Gly Lys Ile Asn Ser Ser Ile Arg Ser Ser
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 Arg Ile Gly Leu Phe Ser Lys Pro Pro Pro Gly Leu Pro Ala Pro Arg
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 Lys Glu Glu Ala Pro Ser Ile Arg Trp Arg Lys Gly Glu Leu Ile Gly
 60 65 70 75
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Lys	Glu	Lys	Thr	Gln	Gly	His	Ile	Arg	Glu	Leu	Glu	Glu	Glu	Val	Gln		
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gta	aga	gag	agt	gat	tcg	ttg	aat	att	ttg	atg	gag	ttt	gtt	cct	ggt	484	
Val	Arg	Glu	Ser	Asp	Ser	Leu	Asn	Ile	Leu	Met	Glu	Phe	Val	Pro	Gly		
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gtc	gat	aac	aaa	ggt	tgc	atc	aga	ctc	gca	gat	ttt	ggt	gct	tcc	aag	676	
Val	Asp	Asn	Lys	Gly	Cys	Ile	Arg	Leu	Ala	Asp	Phe	Gly	Ala	Ser	Lys		
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aaa	gtt	gta	gag	cta	gct	act	gta	aat	ggt	gcc	aaa	tct	atg	aag	ggg	724	
Lys	Val	Val	Glu	Leu	Ala	Thr	Val	Asn	Gly	Ala	Lys	Ser	Met	Lys	Gly		
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Thr	Pro	Tyr	Trp	Met	Ala	Pro	Glu	Val	Ile	Leu	Gln	Thr	Gly	His	Ser		
				240					245					250			
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Phe	Ser	Ala	Asp	Ile	Trp	Ser	Val	Gly	Cys	Thr	Val	Ile	Glu	Met	Ala		
			255					260					265				
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ctt	cat	att	ggt	aga	aca	aaa	gct	cat	cct	cca	att	cca	gaa	gac	ctc	916	
Leu	His	Ile	Gly	Arg	Thr	Lys	Ala	His	Pro	Pro	Ile	Pro	Glu	Asp	Leu		
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tca	cca	gag	gct	aaa	gac	ttt	cta	atg	aaa	tgc	tta	cac	aaa	gaa	cca	964	
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Gly Lys Arg Gln Glu Pro Tyr Pro Ala Tyr Arg Asn Ser Leu Thr Glu	335	340	345	
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Cys Gly Asn Pro Ile Thr Thr Gln Gly Met Asn Val Arg Ser Ser Ile	350	355	360	
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Asn Ser Leu Ile Arg Arg Ser Thr Cys Ser Gly Leu Lys Asp Val Cys	365	370	375	
gaa ctg gga agc ttg agg agt tcc att ata tac cca cag aag tca aat				1204
Glu Leu Gly Ser Leu Arg Ser Ser Ile Ile Tyr Pro Gln Lys Ser Asn	380	385	390	395
aac tca gga ttt ggt tgg cga gat gga gac tct gat gac ctt tgt cag				1252
Asn Ser Gly Phe Gly Trp Arg Asp Gly Asp Ser Asp Asp Leu Cys Gln	400	405	410	
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Thr Asp Met Asp Asp Leu Cys Asn Ile Glu Ser Val Arg Asn Asn Val	415	420	425	
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Leu Ser Gln Ser Thr Asp Leu Asn Lys Ser Phe Asn Pro Met Cys Asp	430	435	440	
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Ser Thr Asp Asn Trp Ser Cys Lys Phe Asp Glu Ser Pro Lys Val Met	445	450	455	
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Lys Ser Lys Ser Asn Leu Leu Ser Tyr Gln Ala Ser Gln Leu Gln Thr	460	465	470	475
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Gly Val Pro Cys Asp Glu Glu Thr Ser Leu Thr Phe Ala Gly Gly Ser	480	485	490	
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Ser Val Ala Glu Asp Asp Tyr Lys Gly Thr Glu Leu Lys Ile Lys Ser	495	500	505	
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Phe Leu Asp Glu Lys Ala Gln Asp Leu Lys Arg Leu Gln Thr Pro Leu	510	515	520	
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Leu Glu Glu Phe His Asn Ala Met Asn Pro Gly Ile Pro Gln Gly Ala	525	530	535	

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gct atg ccc agc cca ctc aaa agc tcc aaa cgt aca ctg aac aca agc 1780
Ala Met Pro Ser Pro Leu Lys Ser Ser Lys Arg Thr Leu Asn Thr Ser
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Arg Val Met Gln Ser Gly Thr Glu Pro Thr Gln Val Asn Glu Ser Thr
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 225 230 235 240
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 325 330 335
 Pro Tyr Pro Ala Tyr Arg Asn Ser Leu Thr Glu Cys Gly Asn Pro Ile
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 355 360 365
 Arg Ser Thr Cys Ser Gly Leu Lys Asp Val Cys Glu Leu Gly Ser Leu
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 Arg Ser Ser Ile Ile Tyr Pro Gln Lys Ser Asn Asn Ser Gly Phe Gly
 385 390 395 400

Trp Arg Asp Gly Asp Ser Asp Asp Leu Cys Gln Thr Asp Met Asp Asp
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 Asp Leu Asn Lys Ser Phe Asn Pro Met Cys Asp Ser Thr Asp Asn Trp
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 Asn Ser Arg Cys Phe Ser Glu Ile Arg Arg Lys Trp Glu Glu Glu Leu
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 Tyr Glu Glu Leu Glu Arg His Arg Glu Asn Leu Arg His Ala Gly Ala
 625 630 635 640
 Gly Gly Lys Thr Pro Leu Ser Gly His Lys Gly
 645 650

<210> 35

<211> 1736

<212> DNA

<213> Arabidopsis thaliana

<220>

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<222> (1)..(1605)

<400> 35

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Met	Pro	Pro	Pro	Lys	Met	Leu	Pro	Pro	Thr	Ala	Arg	Asp	Ser	Val	Ala	
1				5					10					15		
ggg	aca	ggg	ggt	agt	cca	cca	cct	cca	cct	cca	cca	cca	gct	cgg	tgg	96
Gly	Thr	Gly	Gly	Ser	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Arg	Trp	
			20					25					30			
agg	gta	gcg	ggg	gag	gga	gga	ttg	gat	aca	aca	cca	ccg	ccg	ccc	cct	144
Arg	Val	Ala	Gly	Glu	Gly	Gly	Leu	Asp	Thr	Thr	Pro	Pro	Pro	Pro	Pro	
		35					40					45				
cca	acg	gca	gat	aca	gtc	gtg	gcg	gga	agg	acg	agt	tta	ggt	gag	gcg	192
Pro	Thr	Ala	Asp	Thr	Val	Val	Ala	Gly	Arg	Thr	Ser	Leu	Gly	Glu	Ala	
	50					55					60					
ccc	cct	cct	cgt	cag	cct	cca	cgt	cct	cca	aca	gca	cgg	tgg	tca	gcg	240
Pro	Pro	Pro	Arg	Gln	Pro	Pro	Arg	Pro	Pro	Thr	Ala	Arg	Trp	Ser	Ala	
65				70					75					80		
atg	ggc	aga	gtg	atg	tgc	agt	ccg	ccg	ata	cca	cta	tcg	cgg	agt	aga	288
Met	Gly	Arg	Val	Met	Cys	Ser	Pro	Pro	Ile	Pro	Leu	Ser	Arg	Ser	Arg	
				85					90				95			
cta	gcg	ctt	gac	gac	caa	cgt	tgg	ccg	gat	tgg	aca	acg	aac	ggt	tgg	336
Leu	Ala	Leu	Asp	Asp	Gln	Arg	Trp	Pro	Asp	Trp	Thr	Thr	Asn	Gly	Trp	
			100					105					110			
cta	agc	atg	aga	ccg	acg	tcc	tcg	cca	aca	agg	cga	att	gac	cca	caa	384
Leu	Ser	Met	Arg	Pro	Thr	Ser	Ser	Pro	Thr	Arg	Arg	Ile	Asp	Pro	Gln	
		115					120					125				
ggg	gcc	cga	cga	tcc	tca	gtg	tca	cca	gcg	ccg	gtg	aca	acg	ggg	atg	432
Gly	Ala	Arg	Arg	Ser	Ser	Val	Ser	Pro	Ala	Pro	Val	Thr	Thr	Gly	Met	
	130					135					140					
gcc	acc	tct	cgc	act	gac	gat	acg	cta	ata	gag	gca	gag	acc	ggt	cgc	480
Ala	Thr	Ser	Arg	Thr	Asp	Asp	Thr	Leu	Ile	Glu	Ala	Glu	Thr	Gly	Arg	
145					150					155				160		
gac	tgg	acg	agg	aaa	cga	atg	gtc	agg	aaa	ttg	ctt	aaa	gca	agg	gcg	528
Asp	Trp	Thr	Arg	Lys	Arg	Met	Val	Arg	Lys	Leu	Leu	Lys	Ala	Arg	Ala	
				165					170				175			
aaa	gac	tac	aag	gag	ggg	gga	att	gcg	gca	tac	ttt	ggt	tta	cga	gtg	576
Lys	Asp	Tyr	Lys	Glu	Gly	Gly	Ile	Ala	Ala	Tyr	Phe	Gly	Leu	Arg	Val	
			180					185					190			
ctg	cga	tgc	tac	tcg	agg	atc	gta	cga	tcg	atg	aaa	cgc	cca	ggc	aac	624
Leu	Arg	Cys	Tyr	Ser	Arg	Ile	Val	Arg	Ser	Met	Lys	Arg	Pro	Gly	Asn	
		195					200					205				
ttg	aaa	ttc	acg	tgc	cgg	agg	gat	gtg	gca	ata	gcc	acg	ttc	agc	ggc	672
Leu	Lys	Phe	Thr	Cys	Arg	Arg	Asp	Val	Ala	Ile	Ala	Thr	Phe	Ser	Gly	

210	215	220	
aca ggc aga atg cag ctg agt atg aac agc cgt ttg cga gtc gag agc			720
Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser			
225	230	235	240
ctc gtg tcc gcg ggc cag agc gtg gcg tca ttc tgc ctt ttc ctg ata			768
Leu Val Ser Ala Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile			
	245	250	255
tgc acg gcg ccc tcg gcg atg cgg ctg gtt agc ctt ctt aca ctg acc			816
Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr			
	260	265	270
cca agc atg acc tac cta aca tgc ggg ctg gga tgg atg acc gtc gtc			864
Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val			
	275	280	285
gta ctg ccg gcg ata gtg gtc cac tgt tat atg cgc cga cat acg gaa			912
Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu			
	290	295	300
ggg gga tgg ccg tat gcg gca ctc gag gag cat aag acg gag ccg gga			960
Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly			
	305	310	315
cga aat gaa aag atc acc ccg agt aga cgc aac tcg gcg ttc ggc ggc			1008
Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly			
	325	330	335
ctg gtc ggt cga aat aaa aga cga aag aag tcc aag gtc tcc ggc gca			1056
Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala			
	340	345	350
ccg aca gcg gtt tac aca gcg atg ttt ttc atg ttc tcc acg gca atc			1104
Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile			
	355	360	365
aag ggg atg gtg gtg tgc aca atg aaa aaa aaa gtc aaa aaa agt gcg			1152
Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala			
	370	375	380
aat cgc aga ctc gcg cag ttg ctc cga tgg gcg cga tac cac gcg aac			1200
Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn			
	385	390	395
gcg ttc ttg ctc tgt tct ctt gca tgc gca cga ttc gcg gca tcg cga			1248
Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg			
	405	410	415
acg gtc atc cat tgc agt att tac cca cgt ttc ggc ccc tta gcc acg			1296
Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr			
	420	425	430
gtg acg gcc ata tgt ttg ata cta cac acg tgt acg tac cga cgt acg			1344
Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr			
	435	440	445

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gag gca gac acg acg cga cac gaa aat gac gac gcc cgg aag gtg atg 1392
Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met
    450                455                460

gaa gac atg gcc aaa cga atg gac gat agt agc agt ggg agc acg ttg 1440
Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu
465                470                475                480

agc acg ctc acg act gac gag acg tac cac acc acc acg gag gtg acc 1488
Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr
    485                490                495

gat ttt gat tca tct cca tcg tgg gga cga tgc tca tcg cgg cgc ccg 1536
Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro
    500                505                510

ccg gcg ctg ctg gaa tcg aca ttt cgg cga tcc ccg aga ggg tcg acg 1584
Pro Ala Leu Leu Glu Ser Thr Phe Arg Arg Ser Pro Arg Gly Ser Thr
    515                520                525

gga cga cga tgg cga gag tag attcggagtc aggaacgttg gaccgacagg 1635
Gly Arg Arg Trp Arg Glu
    530                535

tggaccgggtt tagggcagtt gacggtaggg gttgcctgac cagccttgac gctcgacagc 1695

taaaaaaaaaac caacaaaaaaaa aaaaaaaaaaac aaaaaaaaaa a 1736

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 <213> Arabidopsis thaliana

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Gly Thr Gly Gly Ser Pro Pro Pro Pro Pro Pro Pro Pro Ala Arg Trp
                20                25                30

Arg Val Ala Gly Glu Gly Gly Leu Asp Thr Thr Pro Pro Pro Pro Pro
  35                40                45

Pro Thr Ala Asp Thr Val Val Ala Gly Arg Thr Ser Leu Gly Glu Ala
  50                55                60

Pro Pro Pro Arg Gln Pro Pro Arg Pro Pro Thr Ala Arg Trp Ser Ala
  65                70                75                80

Met Gly Arg Val Met Cys Ser Pro Pro Ile Pro Leu Ser Arg Ser Arg
                85                90                95

Leu Ala Leu Asp Asp Gln Arg Trp Pro Asp Trp Thr Thr Asn Gly Trp
    100                105                110

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Leu Ser Met Arg Pro Thr Ser Ser Pro Thr Arg Arg Ile Asp Pro Gln
 115 120 125
 Gly Ala Arg Arg Ser Ser Val Ser Pro Ala Pro Val Thr Thr Gly Met
 130 135 140
 Ala Thr Ser Arg Thr Asp Asp Thr Leu Ile Glu Ala Glu Thr Gly Arg
 145 150 155 160
 Asp Trp Thr Arg Lys Arg Met Val Arg Lys Leu Leu Lys Ala Arg Ala
 165 170 175
 Lys Asp Tyr Lys Glu Gly Gly Ile Ala Ala Tyr Phe Gly Leu Arg Val
 180 185 190
 Leu Arg Cys Tyr Ser Arg Ile Val Arg Ser Met Lys Arg Pro Gly Asn
 195 200 205
 Leu Lys Phe Thr Cys Arg Arg Asp Val Ala Ile Ala Thr Phe Ser Gly
 210 215 220
 Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser
 225 230 235 240
 Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile
 245 250 255
 Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr
 260 265 270
 Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val
 275 280 285
 Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu
 290 295 300
 Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly
 305 310 315 320
 Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly
 325 330 335
 Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala
 340 345 350
 Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile
 355 360 365
 Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala
 370 375 380
 Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn
 385 390 395 400
 Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg
 405 410 415

Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr
 420 425 430
 Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr
 435 440 445
 Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met
 450 455 460
 Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu
 465 470 475 480
 Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr
 485 490 495
 Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro
 500 505 510
 Pro Ala Leu Leu Glu Ser Thr Phe Arg Arg Ser Pro Arg Gly Ser Thr
 515 520 525
 Gly Arg Arg Trp Arg Glu
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 1 5 10
 gct aag aag ggt gcc aac ctc ttc aag gtacgaacag agcaaagatg 97
 Ala Lys Lys Gly Ala Asn Leu Phe Lys
 15 20
 ccgctgaaaa ttctcacggc gcattctatc ccgcagaact tttctgacca ctttgtag 155
 acc cgc tgc gct cag tgc cac acc ctg aag gcc ggc gag ggc aac aag 203
 Thr Arg Cys Ala Gln Cys His Thr Leu Lys Ala Gly Glu Gly Asn Lys
 25 30 35

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att ggc cct gag ctc cac ggt ctc ttc ggc cgc aag act ggt tcc gtc 251
Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys Thr Gly Ser Val
      40                      45                      50

gct ggc tac tca tac acc gac gcc aac aag cag aag ggt atc gag tgg 299
Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys Gly Ile Glu Trp
      55                      60                      65

aag gac gac act ctc gtacgtcacg ccaccggaag attgaaatgt ccccgagacc 354
Lys Asp Asp Thr Leu
      70

ctccgctaac acgacacag ttc gag tac ctc gag aac ccc aag aag tac att 406
      Phe Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile
              75                      80

ccc ggt acc aag atg gcc ttc ggt ggt ctc aag aag ccc aag gac cgc 454
Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys Pro Lys Asp Arg
      85                      90                      95                      100

aac gac ctc atc acc ttc ctt gag gag gag acc aaa taa gcgtcttgct 503
Asn Asp Leu Ile Thr Phe Leu Glu Glu Glu Thr Lys
      105                      110

acccc 508

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<210> 38
 <211> 112
 <212> PRT
 <213> Arabidopsis thaliana

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Asn Leu Phe Lys Thr Arg Cys Ala Gln Cys His Thr Leu Lys Ala Gly
      20                      25                      30

Glu Gly Asn Lys Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys
      35                      40                      45

Thr Gly Ser Val Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys
      50                      55                      60

Gly Ile Glu Trp Lys Asp Asp Thr Leu Phe Glu Tyr Leu Glu Asn Pro
      65                      70                      75                      80

Lys Lys Tyr Ile Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys
      85                      90                      95

Pro Lys Asp Arg Asn Asp Leu Ile Thr Phe Leu Glu Glu Glu Thr Lys
      100                      105                      110

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<210> 39
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 1 5 10 15

tta atc aga act cca caa aca aaa caa cgt ctc aat ttc cac tca aaa 96
 Leu Ile Arg Thr Pro Gln Thr Lys Gln Arg Leu Asn Phe His Ser Lys
 20 25 30

acc cca aac cca gac gga tct aaa gat cca tct cca ccg gag cat cca 144
 Thr Pro Asn Pro Asp Gly Ser Lys Asp Pro Ser Pro Pro Glu His Pro
 35 40 45

77

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gtt gaa gta atc ggc cgg atc cga gat tac cct gac cgg aaa gag aaa 192
Val Glu Val Ile Gly Arg Ile Arg Asp Tyr Pro Asp Arg Lys Glu Lys
    50                55                60

tca cct tcg atc tta caa gtc aac aca gat aat caa acg gta cga gtc 240
Ser Pro Ser Ile Leu Gln Val Asn Thr Asp Asn Gln Thr Val Arg Val
    65                70                75                80

aga gct gat gtt ggg tac aga gac ttc aca ctc gac ggt gtt tct ttc 288
Arg Ala Asp Val Gly Tyr Arg Asp Phe Thr Leu Asp Gly Val Ser Phe
                85                90                95

tcg gag caa gaa ggt ctt gaa gag ttc tac aag aag ttt ata gaa gag 336
Ser Glu Gln Glu Gly Leu Glu Glu Phe Tyr Lys Lys Phe Ile Glu Glu
                100                105                110

agg att aaa gga gtg aaa gtt ggg aat aaa tgc acg att atg atg tat 384
Arg Ile Lys Gly Val Lys Val Gly Asn Lys Cys Thr Ile Met Met Tyr
                115                120                125

gga cct act ggt gct gga aag agt cat act atg ttt ggt tgt ggg aaa 432
Gly Pro Thr Gly Ala Gly Lys Ser His Thr Met Phe Gly Cys Gly Lys
                130                135                140

gag cct ggg att gtg tat cgt tct ttg aga gat ata ttg gga gat tct 480
Glu Pro Gly Ile Val Tyr Arg Ser Leu Arg Asp Ile Leu Gly Asp Ser
145                150                155                160

gat caa gat ggt gtt act ttt gtt caa gtt act gtt ctt gag gtt tat 528
Asp Gln Asp Gly Val Thr Phe Val Gln Val Thr Val Leu Glu Val Tyr
                165                170                175

aat gag gag att tat gat ctt ctt tcg act aat agt agt aac aat tta 576
Asn Glu Glu Ile Tyr Asp Leu Leu Ser Thr Asn Ser Ser Asn Asn Leu
                180                185                190

ggg att ggt tgg cct aaa gga gca agc act aag gtaaagtgtt ttgattgata 629
Gly Ile Gly Trp Pro Lys Gly Ala Ser Thr Lys
                195                200

acttttagtat acattgaatt ggctttaaaag gtgtgtactt tgttggtttg ttacag gtg 688
Val

agg ctt gaa gta atg ggg aaa aag gcg aaa aac gca agt ttt att tct 736
Arg Leu Glu Val Met Gly Lys Lys Ala Lys Asn Ala Ser Phe Ile Ser
205                210                215                220

ggg aca gag gct ggg aag att tct aaa gaa att gtc aaa gtg gag aaa 784
Gly Thr Glu Ala Gly Lys Ile Ser Lys Glu Ile Val Lys Val Glu Lys
                225                230                235

cgg aga att gtg aag agt aca ctt tgt aac gaa aga agt tct cgg agt 832
Arg Arg Ile Val Lys Ser Thr Leu Cys Asn Glu Arg Ser Ser Arg Ser
                240                245                250

cac tgc att gtaagaacga tcttcttgat tgatgtgtat gcatagcttt 881

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His Cys Ile
255

atgcagctta tctctgtttt aacttactag tgtgggtggt tcttttttgta g atc ata 938
Ile Ile

ctt gat gtg cca act gtt ggg gga aga ttg atg ctt gtt gac atg gct 986
Leu Asp Val Pro Thr Val Gly Gly Arg Leu Met Leu Val Asp Met Ala
260 265 270

ggg tct gaa aat ata gac caa gct ggg cag act gga ttt gaa gct aag 1034
Gly Ser Glu Asn Ile Asp Gln Ala Gly Gln Thr Gly Phe Glu Ala Lys
275 280 285

atg caa gtaatgtttc ctctctcaat ttgtttgatt ctactaaagt tattgtagtt 1090
Met Gln
290

atggatatca actgacttat atctctcatt attcaacag act gct aag atc aac 1144
Thr Ala Lys Ile Asn
295

cag gga aat att gca ctg aag cga gtt gtg gaa tct ata gca aat gga 1192
Gln Gly Asn Ile Ala Leu Lys Arg Val Val Glu Ser Ile Ala Asn Gly
300 305 310

gat tct cat gta ccc ttt aga gac agc aag ctg acc atg ctt ctc cag 1240
Asp Ser His Val Pro Phe Arg Asp Ser Lys Leu Thr Met Leu Leu Gln
315 320 325

gtgaaattct tgttccattg ttttatcttc tggaaaatgt tttacgtggt gcttggtttt 1300

cttgaagata tttagtgttg tttctattct ctgaatgcag gac tct ttt gaa gat 1355
Asp Ser Phe Glu Asp
330

gac aag tca aag att cta atg atc ctg tgt gcg agc ccg gat cca aag 1403
Asp Lys Ser Lys Ile Leu Met Ile Leu Cys Ala Ser Pro Asp Pro Lys
335 340 345

gaa atg cac aag act ctc tgt act cta gag tat ggg gca aaa gca aag 1451
Glu Met His Lys Thr Leu Cys Thr Leu Glu Tyr Gly Ala Lys Ala Lys
350 355 360 365

tgc ata gtt cgt ggg tct cat act cca aac aaa gat aag tat ggg ggt 1499
Cys Ile Val Arg Gly Ser His Thr Pro Asn Lys Asp Lys Tyr Gly Gly
370 375 380

gat gag tct gct tct gct gtg att ttg gga tca aga ata gct gcc atg 1547
Asp Glu Ser Ala Ser Ala Val Ile Leu Gly Ser Arg Ile Ala Ala Met
385 390 395

gat gag ttc att atc aaa ctc cag tct gag aag aag caa aaa gaa aaa 1595
Asp Glu Phe Ile Ile Lys Leu Gln Ser Glu Lys Lys Gln Lys Glu Lys
400 405 410

gaa agg aat gag gca caa aag cag ctg aag aag aag gaa gag gaa gtt 1643

74

Glu Arg Asn Glu Ala Gln Lys Gln Leu Lys Lys Lys Glu Glu Glu Val	
415 420 425	
gct gct tta aga tct ctt tta aca cag agg gaa gct tgt gct acc aat	1691
Ala Ala Leu Arg Ser Leu Leu Thr Gln Arg Glu Ala Cys Ala Thr Asn	
430 435 440 445	
gaa gag gag ata aaa gag aaa gta aac gag aga acc cag ctt ttg aag	1739
Glu Glu Glu Ile Lys Glu Lys Val Asn Glu Arg Thr Gln Leu Leu Lys	
450 455 460	
tcg gaa cta gat aag aaa ctt gaa gaa tgc cga aga atg gct gag gaa	1787
Ser Glu Leu Asp Lys Lys Leu Glu Glu Cys Arg Arg Met Ala Glu Glu	
465 470 475	
ttt gtt gag atg gag aga agg aga atg gag gaa agg ata gtt cag cag	1835
Phe Val Glu Met Glu Arg Arg Met Glu Glu Arg Ile Val Gln Gln	
480 485 490	
caa gag gaa ctg gag atg atg agg aga cgg tta gag gaa atc gag gtt	1883
Gln Glu Glu Leu Glu Met Met Arg Arg Arg Leu Glu Glu Ile Glu Val	
495 500 505	
gag ttc cgc cgc tca aat gga gga agt gtt gat gaa act agt ggg ttt	1931
Glu Phe Arg Arg Ser Asn Gly Gly Ser Val Asp Glu Thr Ser Gly Phe	
510 515 520 525	
gcc aaa aga ctc agg agt ctt tac tct gat gat gat cct ggt atg gtg	1979
Ala Lys Arg Leu Arg Ser Leu Tyr Ser Asp Asp Asp Pro Gly Met Val	
530 535 540	
aag tca atg gac ctt gac atg ggt gat cca gaa cct gtc aag caa gtg	2027
Lys Ser Met Asp Leu Asp Met Gly Asp Pro Glu Pro Val Lys Gln Val	
545 550 555	
tgg gga gct gtt tca cac caa tca agc aac act att agt agc aac ttc	2075
Trp Gly Ala Val Ser His Gln Ser Ser Asn Thr Ile Ser Ser Asn Phe	
560 565 570	
act aac ctt ttg caa ccg aag cct tca gag aat atg ctt aca cag atg	2123
Thr Asn Leu Leu Gln Pro Lys Pro Ser Glu Asn Met Leu Thr Gln Met	
575 580 585	
tat cct gac cgg gta tgc ttg agc act gtc ttt gaa gaa gaa gaa gtt	2171
Tyr Pro Asp Arg Val Cys Leu Ser Thr Val Phe Glu Glu Glu Glu Val	
590 595 600 605	
gaa gaa gag gaa gaa aaa gtg ata gtc gag gat aaa agc atc tgc ttg	2219
Glu Glu Glu Glu Glu Lys Val Ile Val Glu Asp Lys Ser Ile Cys Leu	
610 615 620	
ata aca aca cca atg cct agt ttg aac tct gaa ggt ttg ggt aaa gag	2267
Ile Thr Thr Pro Met Pro Ser Leu Asn Ser Glu Gly Leu Gly Lys Glu	
625 630 635	
aac tgc ttc aac ggt gca gat gac aag gaa tca gcc tcg tct aga agg	2315
Asn Cys Phe Asn Gly Ala Asp Asp Lys Glu Ser Ala Ser Ser Arg Arg	

640	645	650	
ttg aga att caa aac att ttc acc ctt tgt ggc aat cag aga gag ctg			2363
Leu Arg Ile Gln Asn Ile Phe Thr Leu Cys Gly Asn Gln Arg Glu Leu			
655	660	665	
tct caa cac agt gga cag gag gag gat caa gcc aat att gca tca cct			2411
Ser Gln His Ser Gly Gln Glu Glu Asp Gln Ala Asn Ile Ala Ser Pro			
670	675	680	685
gat aag aaa gac aat cag ttc ttt tct att acg aat aag gcc gaa gca			2459
Asp Lys Lys Asp Asn Gln Phe Phe Ser Ile Thr Asn Lys Ala Glu Ala			
	690	695	700
cta gca gta gaa gaa gca aag gaa aac aat atc tca gtc gat caa agg			2507
Leu Ala Val Glu Glu Ala Lys Glu Asn Asn Ile Ser Val Asp Gln Arg			
	705	710	715
gaa aac ggt cag cta gat atc tat gtt aaa tgg gaa aca gct gct gat			2555
Glu Asn Gly Gln Leu Asp Ile Tyr Val Lys Trp Glu Thr Ala Ala Asp			
	720	725	730
aac cct cga aag ctc ata aca aca ctg aga gtt aca aag gat gca aca			2603
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			20					25					30		
Gly	Lys	Asp	Gly	Trp	Val	Pro	Thr	Pro	Ser	Glu	Asp	Tyr	Ser	His	Trp
		35					40					45			
Ser	His	Arg	Asn	Arg	Phe	Gln	Val	Asn	Asp	Thr	Leu	His	Phe	Lys	Tyr
	50					55					60				
Ala	Lys	Gly	Lys	Asp	Ser	Val	Leu	Glu	Val	Thr	Glu	Gln	Glu	Tyr	Asn
65					70					75					80
Thr	Cys	Asn	Thr	Thr	His	Pro	Leu	Thr	Ser	Leu	Ser	Asp	Gly	Asp	Ser
				85					90					95	
Leu	Phe	Leu	Leu	Ser	His	Ser	Gly	Ser	Tyr	Phe	Phe	Ile	Ser	Gly	Asn
			100					105					110		
Ser	Gln	Asn	Cys	Leu	Lys	Gly	Gln	Lys	Leu	Ala	Val	Lys	Val	Leu	Ser
		115					120					125			

Thr	Val	His	His	Ser	His	Ser	Pro	Arg	His	Thr	Ser	Pro	Ser	Pro	Ser	130	135	140
Pro	Val	His	Gln	Glu	Leu	Ser	Ser	Pro	Gly	Pro	Ser	Pro	Gly	Val	Glu	145	150	155
Pro	Ser	Ser	Asp	Ser	Asn	Ser	Arg	Val	Pro	Ala	Pro	Gly	Pro	Ala	Thr	165	170	175
Ala	Pro	Asn	Ser	Ala	Gly	Leu	Val	Gly	Pro	Gly	Met	Val	Val	Leu	Val	180	185	190
Val	Asn	Ser	Ile	Ile	Lys	Pro	Ile	Asp	Ser	Phe	Leu	Leu	Lys	Ser	Leu	195	200	205
Pro	Leu	Val	Val	Asp	Val	Ala	Val	Gly	Ile	Ser	Thr	Ser	Arg	Gln	Leu	210	215	220
Gln	Ala	Ser	Glu	Glu	Pro	Val	Ser	Ser	Pro	Leu	Ser	Ser	Pro	Ala	Leu	225	230	235
Leu	Gly	Ser	Gly	Lys	Glu	Glu	Glu	Gln	Lys	Ile	Ile	Pro	Lys	Arg	Gln	245	250	255
Lys	Val	Gln	Ala	Val	Leu	Lys	Ser	Ile	Lys	Gln	Ser	Pro	Lys	Lys	Val	260	265	270
Asn	Leu	Val	Ala	Ala	Leu	Val	Arg	Gly	Met	Arg	Val	Glu	Asp	Ala	Leu	275	280	285
Ile	Gln	Leu	Gln	Val	Thr	Val	Lys	Arg	Ala	Ala	Gln	Thr	Val	Tyr	Arg	290	295	300
Val	Ile	His	Ala	Ala	Arg	Ala	Asn	Ala	Thr	His	Asn	His	Gly	Leu	Asp	305	310	315
Pro	Asp	Arg	Leu	Leu	Val	Ala	Glu	Ala	Phe	Val	Gly	Lys	Gly	Leu	Phe	325	330	335
Gly	Lys	Lys	Val	Ala	Tyr	His	Ala	Lys	Gly	Arg	Ser	Gly	Ile	Ile	Ser	340	345	350
Ile	Pro	Arg	Cys	Arg	Leu	Thr	Val	Ile	Val	Arg	Glu	Thr	Thr	Pro	Glu	355	360	365
Glu	Glu	Ala	Glu	Ile	Ala	Arg	Leu	Lys	Val	His	Asn	Phe	Lys	Lys	Lys	370	375	380
Ser	Lys	Arg	Glu	Arg	Gln	Leu	Val	Pro	His	Lys	Leu	Ile	Glu	Thr	Ser	385	390	395
Pro	Ile	Trp	Asn	Arg	Arg	Gly	Thr	Lys	Ala	Asn	His	Arg	Ser	Ser	Glu	405	410	415
Leu	Val	Leu	Thr	Ile	Ile	Leu	Asp	Val	Thr	Cys	Val	Gly	Asn	Met	Glu	420	425	430

Lys Asn Arg Leu Asp Asn Leu Thr Asn Gln Asn Asn Ile Tyr His His
 435 440 445
 Asn Pro Glu Glu Thr Cys Ser Phe Arg Cys Asn Gly Ser Glu Arg Ile
 450 455 460
 Asp Val Asp Ala Asp Val Val Val Val Asp Val Val Glu Leu Leu Val
 465 470 475 480
 Ser Glu Asn Ile Glu Phe Asn Gly Glu Asp Ser Ala Ile Gly Val Thr
 485 490 495
 Val Ile Gly Glu Val Glu Glu Ala Glu Met Leu Arg
 500 505

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 <213> Arabidopsis thaliana

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 <222> (26)..(718)

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 Met Phe Ala Asn Lys Phe Pro Gly Val
 1 5

 tac gca gcc act tgt ctc tcc gtc gaa gac gcc gtc aac gct cga tca 100
 Tyr Ala Ala Thr Cys Leu Ser Val Glu Asp Ala Val Asn Ala Arg Ser
 10 15 20 25

 ata agc aat tgc aat gtc ctc gca ttc tcc ggc atc aaa aca tcc ccg 148
 Ile Ser Asn Cys Asn Val Leu Ala Phe Ser Gly Ile Lys Thr Ser Pro
 30 35 40

 gaa acc gcc ttg gaa atc ttc gac gct tgg atc aaa act cct ttc aaa 196
 Glu Thr Ala Leu Glu Ile Phe Asp Ala Trp Ile Lys Thr Pro Phe Lys
 45 50 55

 tct cct tgt cct gcg tcc gga tcc gaa cca tgg agc tca gtt atc tct 244
 Ser Pro Cys Pro Ala Ser Gly Ser Glu Pro Trp Ser Ser Val Ile Ser
 60 65 70

 tcc ttc ctc gac aat tct ctc tcc gag atg tct cag att gga aag tca 292
 Ser Phe Leu Asp Asn Ser Leu Ser Glu Met Ser Gln Ile Gly Lys Ser
 75 80 85

 acc gcc ggc gat tca aca acc aag aag atc gat gaa aca acc gcg tct 340
 Thr Ala Gly Asp Ser Thr Thr Lys Lys Ile Asp Glu Thr Thr Ala Ser
 90 95 100 105

 tgc gta att tgc tgc ttg gcg aag aac aga gag ttc act cca gtg gac 388

Cys Val Ile Cys Cys Leu Ala Lys Asn Arg Glu Phe Thr Pro Val Asp
 110 115 120
 atc atg ccg gga ggc tcg atg aag atc gtt aga gag acg ccg acg tcg 436
 Ile Met Pro Gly Gly Ser Met Lys Ile Val Arg Glu Thr Pro Thr Ser
 125 130 135
 gcg att gta aga ttc aaa gcg gga agt gtg gaa ccg gcg cat cac cac 484
 Ala Ile Val Arg Phe Lys Ala Gly Ser Val Glu Pro Ala His His His
 140 145 150
 aca ttc ggc cat gac ctt gta gtc ata aag gga aag aaa agt gtg tgg 532
 Thr Phe Gly His Asp Leu Val Val Ile Lys Gly Lys Lys Ser Val Trp
 155 160 165
 aat ctg agc aag aag gag aga gct gat ctc gtt gac ggc gat tac cta 580
 Asn Leu Ser Lys Lys Glu Arg Ala Asp Leu Val Asp Gly Asp Tyr Leu
 170 175 180 185
 ttc act ccc gcc ggt gat gtt cac cga gtc aaa tat cac gaa gac act 628
 Phe Thr Pro Ala Gly Asp Val His Arg Val Lys Tyr His Glu Asp Thr
 190 195 200
 gag ttc ttc atc act tgg gat ggc cat tgg gac ata ttc ctt gac gaa 676
 Glu Phe Phe Ile Thr Trp Asp Gly His Trp Asp Ile Phe Leu Asp Glu
 205 210 215
 gac ctc gaa act gca aag aaa gcc atc gaa gaa gaa gct tga 718
 Asp Leu Glu Thr Ala Lys Lys Ala Ile Glu Glu Glu Ala
 220 225 230
 aggtgtaaac t 729

<210> 44
 <211> 230
 <212> PRT
 <213> Arabidopsis thaliana

<400> 44
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 Val Glu Asp Ala Val Asn Ala Arg Ser Ile Ser Asn Cys Asn Val Leu
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 Ala Phe Ser Gly Ile Lys Thr Ser Pro Glu Thr Ala Leu Glu Ile Phe
 35 40 45
 Asp Ala Trp Ile Lys Thr Pro Phe Lys Ser Pro Cys Pro Ala Ser Gly
 50 55 60
 Ser Glu Pro Trp Ser Ser Val Ile Ser Ser Phe Leu Asp Asn Ser Leu
 65 70 75 80
 Ser Glu Met Ser Gln Ile Gly Lys Ser Thr Ala Gly Asp Ser Thr Thr
 85 90 95

Lys Lys Ile Asp Glu Thr Thr Ala Ser Cys Val Ile Cys Cys Leu Ala
 100 105 110
 Lys Asn Arg Glu Phe Thr Pro Val Asp Ile Met Pro Gly Gly Ser Met
 115 120 125
 Lys Ile Val Arg Glu Thr Pro Thr Ser Ala Ile Val Arg Phe Lys Ala
 130 135 140
 Gly Ser Val Glu Pro Ala His His His Thr Phe Gly His Asp Leu Val
 145 150 155 160
 Val Ile Lys Gly Lys Lys Ser Val Trp Asn Leu Ser Lys Lys Glu Arg
 165 170 175
 Ala Asp Leu Val Asp Gly Asp Tyr Leu Phe Thr Pro Ala Gly Asp Val
 180 185 190
 His Arg Val Lys Tyr His Glu Asp Thr Glu Phe Phe Ile Thr Trp Asp
 195 200 205
 Gly His Trp Asp Ile Phe Leu Asp Glu Asp Leu Glu Thr Ala Lys Lys
 210 215 220
 Ala Ile Glu Glu Glu Ala
 225 230

<210> 45
 <211> 1203
 <212> DNA
 <213> Arabidopsis thaliana

<220>
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 <222> (12)..(1193)

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 Met Thr Ile Arg Asn Gln Arg Phe Ser Leu Leu Lys Gln
 1 5 10
 cct ata tcc tcc aca ctt aat cag cat tta gta gat tat cca acc ccg 98
 Pro Ile Ser Ser Thr Leu Asn Gln His Leu Val Asp Tyr Pro Thr Pro
 15 20 25
 agc aat ctt agt tat tgg tgg ggg ttc ggt ccg tta gct ggt att tgt 146
 Ser Asn Leu Ser Tyr Trp Trp Gly Phe Gly Pro Leu Ala Gly Ile Cys
 30 35 40 45
 tta gtc att cag ata gtg act ggc gtt ttt tta gct atg cat tac aca 194
 Leu Val Ile Gln Ile Val Thr Gly Val Phe Leu Ala Met His Tyr Thr
 50 55 60
 cct cat gtg gat tta gct ttc aac agc gta gaa cac att atg aga gat 242

Pro His Val Asp Leu Ala Phe Asn Ser Val Glu His Ile Met Arg Asp	
65 70 75	
ggt gaa ggg ggc tgg ttg ctc cgt tat atg cat gct aat ggg gca agt	290
Val Glu Gly Gly Trp Leu Leu Arg Tyr Met His Ala Asn Gly Ala Ser	
80 85 90	
atg ttt ctt att gtg gtt tac ctt cat att ttt cgt ggt cta tat cat	338
Met Phe Leu Ile Val Val Tyr Leu His Ile Phe Arg Gly Leu Tyr His	
95 100 105	
gcg agt tat agc agt cct agg gaa ttt gtt tgg tgt ctt gga gtt gta	386
Ala Ser Tyr Ser Ser Pro Arg Glu Phe Val Trp Cys Leu Gly Val Val	
110 115 120 125	
atc ttc cta tta atg att gtg aca gct ttt ata gga tat gta cta cct	434
Ile Phe Leu Leu Met Ile Val Thr Ala Phe Ile Gly Tyr Val Leu Pro	
130 135 140	
tgg ggt cag atg agc ttt tgg gga gct aca gta att aca agc tta gct	482
Trp Gly Gln Met Ser Phe Trp Gly Ala Thr Val Ile Thr Ser Leu Ala	
145 150 155	
agc gcc ata cct gta gta gga gat acc ata gtg act tgg ctt tgg ggt	530
Ser Ala Ile Pro Val Val Gly Asp Thr Ile Val Thr Trp Leu Trp Gly	
160 165 170	
ggt ttc tcc gtg gac aat gcc acc tta aat cgt ttt ttt agt ctt cat	578
Gly Phe Ser Val Asp Asn Ala Thr Leu Asn Arg Phe Phe Ser Leu His	
175 180 185	
cat tta ctc ccc ttt att tta gta ggc gcc agt ctt ctt cat ctg gcc	626
His Leu Leu Pro Phe Ile Leu Val Gly Ala Ser Leu Leu His Leu Ala	
190 195 200 205	
gca ttg cat caa tat gga tca aat aat cca ttg ggt gta cat tct gag	674
Ala Leu His Gln Tyr Gly Ser Asn Asn Pro Leu Gly Val His Ser Glu	
210 215 220	
atg gat aaa ata gct ttt tac cct tat ttt tat gtc aag gat cta gtt	722
Met Asp Lys Ile Ala Phe Tyr Pro Tyr Phe Tyr Val Lys Asp Leu Val	
225 230 235	
ggt tgg gta gct ttt gct atc ttt ttt tct att tgg att ttt tat gct	770
Gly Trp Val Ala Phe Ala Ile Phe Phe Ser Ile Trp Ile Phe Tyr Ala	
240 245 250	
cct aat gtt ttg gga cat ccc gac aat tat ata cct gct aat ccg atg	818
Pro Asn Val Leu Gly His Pro Asp Asn Tyr Ile Pro Ala Asn Pro Met	
255 260 265	
tcc acc ccg cct cat att gtg ccg gaa tgg tat ttc cta ccg atc cat	866
Ser Thr Pro Pro His Ile Val Pro Glu Trp Tyr Phe Leu Pro Ile His	
270 275 280 285	
gcc att ctt cgt agt ata cct gac aaa gcg gga ggt gta gcc gca ata	914
Ala Ile Leu Arg Ser Ile Pro Asp Lys Ala Gly Gly Val Ala Ala Ile	

	290	295	300	
gca cca gtt ttt ata tgt ctc ttg gct tta cct ttt ttt aaa agt atg				962
Ala Pro Val Phe Ile Cys Leu Leu Ala Leu Pro Phe Phe Lys Ser Met				
	305	310	315	
tat gtg cgt agt tca agt ttt cga ccg att cac caa gga atg ttt tgg				1010
Tyr Val Arg Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp				
	320	325	330	
ttg ctt ttg gcg gat tgc tta cta cta ggt tgg atc gga tgt caa cct				1058
Leu Leu Leu Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro				
	335	340	345	
gtg gag gct cca ttt gtt act att gga caa att tct cct ttg gtt ttc				1106
Val Glu Ala Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe				
	350	355	360	365
ttc ttg ttc ttt gcc ata acg ccc att ctg gga cga gtt gga aga gga				1154
Phe Leu Phe Phe Ala Ile Thr Pro Ile Leu Gly Arg Val Gly Arg Gly				
	370	375	380	
att cct aat tct tac acg gat gag act gat cac acc tga tcagtgaaaa				1203
Ile Pro Asn Ser Tyr Thr Asp Glu Thr Asp His Thr				
	385	390		

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<211> 393

<212> PRT

<213> Arabidopsis thaliana

<400> 46

Met Thr Ile Arg Asn Gln Arg Phe Ser Leu Leu Lys Gln Pro Ile Ser
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Ser Thr Leu Asn Gln His Leu Val Asp Tyr Pro Thr Pro Ser Asn Leu
20 25 30

Ser Tyr Trp Trp Gly Phe Gly Pro Leu Ala Gly Ile Cys Leu Val Ile
35 40 45

Gln Ile Val Thr Gly Val Phe Leu Ala Met His Tyr Thr Pro His Val
50 55 60

Asp Leu Ala Phe Asn Ser Val Glu His Ile Met Arg Asp Val Glu Gly
65 70 75 80

Gly Trp Leu Leu Arg Tyr Met His Ala Asn Gly Ala Ser Met Phe Leu
85 90 95

Ile Val Val Tyr Leu His Ile Phe Arg Gly Leu Tyr His Ala Ser Tyr
100 105 110

Ser Ser Pro Arg Glu Phe Val Trp Cys Leu Gly Val Val Ile Phe Leu
115 120 125

Leu Met Ile Val Thr Ala Phe Ile Gly Tyr Val Leu Pro Trp Gly Gln
 130 135 140
 Met Ser Phe Trp Gly Ala Thr Val Ile Thr Ser Leu Ala Ser Ala Ile
 145 150 155 160
 Pro Val Val Gly Asp Thr Ile Val Thr Trp Leu Trp Gly Gly Phe Ser
 165 170 175
 Val Asp Asn Ala Thr Leu Asn Arg Phe Phe Ser Leu His His Leu Leu
 180 185 190
 Pro Phe Ile Leu Val Gly Ala Ser Leu Leu His Leu Ala Ala Leu His
 195 200 205
 Gln Tyr Gly Ser Asn Asn Pro Leu Gly Val His Ser Glu Met Asp Lys
 210 215 220
 Ile Ala Phe Tyr Pro Tyr Phe Tyr Val Lys Asp Leu Val Gly Trp Val
 225 230 235 240
 Ala Phe Ala Ile Phe Phe Ser Ile Trp Ile Phe Tyr Ala Pro Asn Val
 245 250 255
 Leu Gly His Pro Asp Asn Tyr Ile Pro Ala Asn Pro Met Ser Thr Pro
 260 265 270
 Pro His Ile Val Pro Glu Trp Tyr Phe Leu Pro Ile His Ala Ile Leu
 275 280 285
 Arg Ser Ile Pro Asp Lys Ala Gly Gly Val Ala Ala Ile Ala Pro Val
 290 295 300
 Phe Ile Cys Leu Leu Ala Leu Pro Phe Phe Lys Ser Met Tyr Val Arg
 305 310 315 320
 Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp Leu Leu Leu
 325 330 335
 Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro Val Glu Ala
 340 345 350
 Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe Phe Leu Phe
 355 360 365
 Phe Ala Ile Thr Pro Ile Leu Gly Arg Val Gly Arg Gly Ile Pro Asn
 370 375 380
 Ser Tyr Thr Asp Glu Thr Asp His Thr
 385 390

<210> 47

<211> 1194

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1194)

<400> 47

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atg aga aaa gtt tct tcc gta att tct gtc gtt gat ccc gtt att ttc      48
Met Arg Lys Val Ser Ser Val Ile Ser Val Val Asp Pro Val Ile Phe
   1               5               10               15

cga gga aat tac gca gct aca ctc gat gtg tcg tat ccg gta ttc ccg      96
Arg Gly Asn Tyr Ala Ala Thr Leu Asp Val Ser Tyr Pro Val Phe Pro
               20               25               30

caa aat aaa gat ggc cgt gca ctt cag aaa gtt ctc gga acc att cgt      144
Gln Asn Lys Asp Gly Arg Ala Leu Gln Lys Val Leu Gly Thr Ile Arg
               35               40               45

aac gga gat ttg gct gtt tcg gct cct aaa aca agt ctt agg gca ggt      192
Asn Gly Asp Leu Ala Val Ser Ala Pro Lys Thr Ser Leu Arg Ala Gly
               50               55               60

att ttc ggt gaa ggt tcc agc ttg gtc gat cag atg ccc tgt aaa gtt      240
Ile Phe Gly Glu Gly Ser Ser Leu Val Asp Gln Met Pro Cys Lys Val
   65               70               75               80

tac gtg gcg ttc cac aaa gaa tca tac tgc tcg ctt acc ggg cta agc      288
Tyr Val Ala Phe His Lys Glu Ser Tyr Cys Ser Leu Thr Gly Leu Ser
               85               90               95

aaa cgc gga gtc gca ata aac gaa gca agt ctt tcc ctg gtc gga atc      336
Lys Arg Gly Val Ala Ile Asn Glu Ala Ser Leu Ser Leu Val Gly Ile
               100              105              110

act aaa gtt aga gcc ccc gtc gga aat acc gtt gga gcg gaa gca acc      384
Thr Lys Val Arg Ala Pro Val Gly Asn Thr Val Gly Ala Glu Ala Thr
               115              120              125

gta tac ata ggt agt cca aaa cct tat aca gag tgt agt act cca aat      432
Val Tyr Ile Gly Ser Pro Lys Pro Tyr Thr Glu Cys Ser Thr Pro Asn
               130              135              140

aaa atg tat gcg gtt gca gct ggt ttc aag gtg gca agt ttc gcc gct      480
Lys Met Tyr Ala Val Ala Ala Gly Phe Lys Val Ala Ser Phe Ala Ala
               145              150              155              160

agt acg tgc gta cgt ccg cct gca cgt gca cgt cgt acg ctg acc gtg      528
Ser Thr Cys Val Arg Pro Pro Ala Arg Ala Arg Arg Thr Leu Thr Val
               165              170              175

acg tcg acc gtg acg ctg tct atg gca act ggt aaa tgc gta aat aca      576
Thr Ser Thr Val Thr Leu Ser Met Ala Thr Gly Lys Cys Val Asn Thr
               180              185              190

gga aac gaa cca gta tct aaa cct aca gga gta cgt atg atg tta att      624
Gly Asn Glu Pro Val Ser Lys Pro Thr Gly Val Arg Met Met Leu Ile
               195              200              205

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cct ctc gat gct act ctc att aaa gta tgg act ggg gaa gta aaa aaa 672
Pro Leu Asp Ala Thr Leu Ile Lys Val Trp Thr Gly Glu Val Lys Lys
    210                      215                      220

gcg ata gtt tcc cgg cct gca aaa att ttc aat agc gta gga aat tta 720
Ala Ile Val Ser Arg Pro Ala Lys Ile Phe Asn Ser Val Gly Asn Leu
225                      230                      235                      240

gaa cgt cct tca att tcg cat tct tgt gga caa ggt ttg gat gaa gct 768
Glu Arg Pro Ser Ile Ser His Ser Cys Gly Gln Gly Leu Asp Glu Ala
    245                      250                      255

gcc gct tat atc aag ggt aga ctt tct cca atc gtt aaa gca gaa aga 816
Ala Ala Tyr Ile Lys Gly Arg Leu Ser Pro Ile Val Lys Ala Glu Arg
    260                      265                      270

att aaa gtt ttg gtt aaa gac gag cac gaa gaa gta aaa gaa ctt ctt 864
Ile Lys Val Leu Val Lys Asp Glu His Glu Glu Val Lys Glu Leu Leu
    275                      280                      285

caa gaa ggt tac gaa gaa atc gtc ggt gag tct cca agt ttc aat tta 912
Gln Glu Gly Tyr Glu Glu Ile Val Gly Glu Ser Pro Ser Phe Asn Leu
    290                      295                      300

gca caa gaa gcg tgg gaa aaa gct gaa aga cga gca aaa ggt cag tcc 960
Ala Gln Glu Ala Trp Glu Lys Ala Glu Arg Arg Ala Lys Gly Gln Ser
305                      310                      315                      320

ccg tgc agt gcg gca aaa gca aac ctt gca acc tac tat ttt tca aca 1008
Pro Cys Ser Ala Ala Lys Ala Asn Leu Ala Thr Tyr Tyr Phe Ser Thr
    325                      330                      335

ggt gat ttc gaa aaa tca att aaa ctc tac gaa gaa cct atg ggt ttg 1056
Gly Asp Phe Glu Lys Ser Ile Lys Leu Tyr Glu Glu Pro Met Gly Leu
    340                      345                      350

aaa gat act gat aag agc tat ctg cga gaa cgt aga aaa aga gta gag 1104
Lys Asp Thr Asp Lys Ser Tyr Leu Arg Glu Arg Arg Lys Arg Val Glu
    355                      360                      365

gct act acg ttg cgt gca ccg ttc gtg gtc cag ctg acc gtg cgt agt 1152
Ala Thr Thr Leu Arg Ala Pro Phe Val Val Gln Leu Thr Val Arg Ser
    370                      375                      380

cgt acg acg atg atc gcc gtt ggt gaa agc aac gca aac tga 1194
Arg Thr Thr Met Ile Ala Val Gly Glu Ser Asn Ala Asn
385                      390                      395

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<210> 48

<211> 397

<212> PRT

<213> Arabidopsis thaliana

<400> 48

Met Arg Lys Val Ser Ser Val Ile Ser Val Val Asp Pro Val Ile Phe

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Arg Gly Asn Tyr	Ala Ala Thr Leu	Asp Val Ser Tyr	Pro Val Phe Pro
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Gln Asn Lys Asp	Gly Arg Ala Leu	Gln Lys Val Leu	Gly Thr Ile Arg
	35	40	45
Asn Gly Asp Leu	Ala Val Ser Ala	Pro Lys Thr Ser	Leu Arg Ala Gly
	50	55	60
Ile Phe Gly Glu	Gly Ser Ser Leu	Val Asp Gln Met	Pro Cys Lys Val
	65	70	75
Tyr Val Ala Phe	His Lys Glu Ser	Tyr Cys Ser Leu	Thr Gly Leu Ser
	85	90	95
Lys Arg Gly Val	Ala Ile Asn Glu	Ala Ser Leu Ser	Leu Val Gly Ile
	100	105	110
Thr Lys Val Arg	Ala Pro Val Gly	Asn Thr Val Gly	Ala Glu Ala Thr
	115	120	125
Val Tyr Ile Gly	Ser Pro Lys Pro	Tyr Thr Glu Cys	Ser Thr Pro Asn
	130	135	140
Lys Met Tyr Ala	Val Ala Ala Gly	Phe Lys Val Ala	Ser Phe Ala Ala
	145	150	155
Ser Thr Cys Val	Arg Pro Pro Ala	Arg Ala Arg Arg	Thr Leu Thr Val
	165	170	175
Thr Ser Thr Val	Thr Leu Ser Met	Ala Thr Gly Lys	Cys Val Asn Thr
	180	185	190
Gly Asn Glu Pro	Val Ser Lys Pro	Thr Gly Val Arg	Met Met Leu Ile
	195	200	205
Pro Leu Asp Ala	Thr Leu Ile Lys	Val Trp Thr Gly	Glu Val Lys Lys
	210	215	220
Ala Ile Val Ser	Arg Pro Ala Lys	Ile Phe Asn Ser	Val Gly Asn Leu
	225	230	235
Glu Arg Pro Ser	Ile Ser His Ser	Cys Gly Gln Gly	Leu Asp Glu Ala
	245	250	255
Ala Ala Tyr Ile	Lys Gly Arg Leu	Ser Pro Ile Val	Lys Ala Glu Arg
	260	265	270
Ile Lys Val Leu	Val Lys Asp Glu	His Glu Glu Val	Lys Glu Leu Leu
	275	280	285
Gln Glu Gly Tyr	Glu Glu Ile Val	Gly Glu Ser Pro	Ser Phe Asn Leu
	290	295	300
Ala Gln Glu Ala	Trp Glu Lys Ala	Glu Arg Arg Ala	Lys Gly Gln Ser

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305                      310                      315                      320
Pro Cys Ser Ala Ala Lys Ala Asn Leu Ala Thr Tyr Tyr Phe Ser Thr
                      325                      330                      335
Gly Asp Phe Glu Lys Ser Ile Lys Leu Tyr Glu Glu Pro Met Gly Leu
                      340                      345                      350
Lys Asp Thr Asp Lys Ser Tyr Leu Arg Glu Arg Arg Lys Arg Val Glu
                      355                      360                      365
Ala Thr Thr Leu Arg Ala Pro Phe Val Val Gln Leu Thr Val Arg Ser
                      370                      375                      380
Arg Thr Thr Met Ile Ala Val Gly Glu Ser Asn Ala Asn
385                      390                      395

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<210> 49
<211> 611
<212> DNA
<213> Arabidopsis thaliana

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<220>
<221> CDS
<222> (5)..(601)

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gtc gtc ttt tcc gtc gcg ctt ctt ctg ttc tac ttc tct gaa act tct 97
Val Val Phe Ser Val Ala Leu Leu Leu Phe Tyr Phe Ser Glu Thr Ser
                      20                      25                      30

cta gga gct cct tgt ccc atc aat ggc ttg cca atc gtg agg aat att 145
Leu Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile
                      35                      40                      45

agt gac ctt cct cag gat aac tat gga aga cca ggt ctt tcc cac atg 193
Ser Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met
                      50                      55                      60

act gtt gct ggc tcc gta ttg cat gga atg aaa gag gtt gaa ata tgg 241
Thr Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp
                      65                      70                      75

ctt cag aca ttt gct cca ggt tca gag aca cca att cac agg cac tcc 289
Leu Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser
                      80                      85                      90                      95

tgt gaa gag gtt ttt gtt gtc cta aag ggc agt ggt act ctg tat ctc 337
Cys Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu
                      100                      105                      110

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Ala Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile
      115              120              125

ttt gcc aac agt aca att cat att ccg atc aat gat gct cat cag gtc 433
Phe Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val
      130              135              140

aaa aac acc ggt cat gag gac ctg cag gtg ttg gtt atc ata tct cgg 481
Lys Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg
      145              150              155

ccg cct att aaa atc ttc atc tac gaa gac tgg ttt atg cca cac act 529
Pro Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr
      160              165              170              175

gct gca agg ctg aag ttc cct tac tat tgg gat gag caa tgc att caa 577
Ala Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile Gln
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Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile Ser
      35              40              45

Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met Thr
      50              55              60

Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp Leu
      65              70              75              80

Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser Cys
      85              90              95

Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu Ala
      100             105             110

Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile Phe
      115             120             125

Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val Lys
      130             135             140

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Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg Pro
 145 150 155 160
 Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr Ala
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 Ser Gln Lys Asp Glu Leu
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 Pro Cys Arg Gly Ala Ser Ile Thr Gly Ser Leu Arg Asp Arg Pro
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 acc gct atc ctt atc gga acc ctc acc gct tta ggc ggt gga gtt aga 144
 Thr Ala Ile Leu Ile Gly Thr Leu Thr Ala Leu Gly Gly Gly Val Arg
 35 40 45
 tgt ggc tct tgc ccc agt gtc gac cgt tgc gga cac gca agt gcc gcc 192
 Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala
 50 55 60
 ata gcg cgt gat agc tgt gcc gtg ttc gca tgg aag cga ggt acg cga 240
 Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg
 65 70 75 80
 caa gag tac tgg tgc tgc act gaa ccg acc ctt gac tgg ggc ccc ggt 288
 Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly
 85 90 95
 ggt gga ccc gac ttc gat tgt gat gat ggt ggt gac gat ccg ctt ttg 336
 Gly Gly Pro Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu
 100 105 110
 att caa gat ggc gta aaa gct gcg gag gaa tat gct aaa tct gga aaa 384
 Ile Gln Asp Gly Val Lys Ala Ala Glu Glu Tyr Ala Lys Ser Gly Lys
 115 120 125

gtt cca gat cca agc tgt act gat aat gct gag ttt caa gtt gtg ctt	432
Val Pro Asp Pro Ser Cys Thr Asp Asn Ala Glu Phe Gln Val Val Leu	
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Ile Ile Ile Arg Glu Gly Leu Lys Thr Asp Pro Leu Lys Tyr Thr Lys	
145 150 155 160	
cga ccc agt tgc ctt gtt ggt gtt tct gag gaa act act act ggt gtt	528
Arg Pro Ser Cys Leu Val Gly Val Ser Glu Glu Thr Thr Thr Gly Val	
165 170 175	
aag aga agt tac caa atg cag ccg aaa tgt act ttg ctt ttg cat gct	576
Lys Arg Ser Tyr Gln Met Gln Pro Lys Cys Thr Leu Leu His Ala	
180 185 190	
act gat gtt tgt gac acc gtg atc aag agc aag att gat aac ttg tac	624
Thr Asp Val Cys Asp Thr Val Ile Lys Ser Lys Ile Asp Asn Leu Tyr	
195 200 205	
gga tgc cgc cac tca ctt tcg gat ggt ctc atg agg gct act gat gtt	672
Gly Cys Arg His Ser Leu Ser Asp Gly Leu Met Arg Ala Thr Asp Val	
210 215 220	
cgt cgc ccc tgc aag gta gcg ctt gta ggc ggt tac gga gat gtc ttt	720
Arg Arg Pro Cys Lys Val Ala Leu Val Gly Gly Tyr Gly Asp Val Phe	
225 230 235 240	
aag ggt tgg gtt gct gcc ttg aag caa gct ggt gca cgt gtc atc gtg	768
Lys Gly Trp Val Ala Ala Leu Lys Gln Ala Gly Ala Arg Val Ile Val	
245 250 255	
act gag atc ccg caa atc tgt gcc gtc caa gct acc atg gaa ggt agt	816
Thr Glu Ile Pro Gln Ile Cys Ala Val Gln Ala Thr Met Glu Gly Ser	
260 265 270	
tcg gtc ctt acc ctt gag gat gtc gtt tca gat gtt gat cgc ttc gtt	864
Ser Val Leu Thr Leu Glu Asp Val Val Ser Asp Val Asp Arg Phe Val	
275 280 285	
acg aca acc ggt aac aag gac ctc atc atg gtt gac cac atg agg cga	912
Thr Thr Thr Gly Asn Lys Asp Leu Ile Met Val Asp His Met Arg Arg	
290 295 300	
atg aag aac cag gcc ata gtt tgc aac att cga cgt ttc gac aat gaa	960
Met Lys Asn Gln Ala Ile Val Cys Asn Ile Arg Arg Phe Asp Asn Glu	
305 310 315 320	
atc gac atg cgc agt ctc gag acc ttc cct gga gtg aag cgg atc aca	1008
Ile Asp Met Arg Ser Leu Glu Thr Phe Pro Gly Val Lys Arg Ile Thr	
325 330 335	
atc aag gcc cag act gac aga tgg gtc ttt cgc gac acc aac aga ggt	1056
Ile Lys Ala Gln Thr Asp Arg Trp Val Phe Arg Asp Thr Asn Arg Gly	
340 345 350	
atc att gtc cca gcc gag ggg cgt ctc atg acg atg gga tgc gcc act	1104

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Ile Ile Val Pro Ala Glu Gly Arg Leu Met Thr Met Gly Cys Ala Thr
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gga cac ccc agc ttc cgg acg tcc tgc tct ttc act aac caa gtc agt 1152
Gly His Pro Ser Phe Arg Thr Ser Cys Ser Phe Thr Asn Gln Val Ser
   370                               375                               380

tct cag ctc gag ttg tgg cgg gag aag agc acc ggc aag tat gag aag 1200
Ser Gln Leu Glu Leu Trp Arg Glu Lys Ser Thr Gly Lys Tyr Glu Lys
   385                               390                               395                               400

aaa gtg tac gtc ttc cca aag cac ctt gag aag aag gtt gcc gcc ctt 1248
Lys Val Tyr Val Phe Pro Lys His Leu Glu Lys Lys Val Ala Ala Leu
                   405                               410                               415

cat ctc gta aag ctc gga gca agg ctc act aag ctt agt cgg tgc acg 1296
His Leu Val Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Arg Cys Thr
                   420                               425                               430

ttg ttg tgc acg gac gac cca gtt gaa ggt cgt aaa gag cct cct cac 1344
Leu Leu Cys Thr Asp Asp Pro Val Glu Gly Arg Lys Glu Pro Pro His
                   435                               440                               445

cgt gct ggc agc cct gaa ccg tgc cag ctg cag ctg acc gtg ttc agg 1392
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465

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Thr Ala Ile Leu Ile Gly Thr Leu Thr Ala Leu Gly Gly Gly Val Arg
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Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala
   50                               55                               60

Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg
   65                               70                               75                               80

Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly
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Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu

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Arg	Pro	Ser	Cys	Leu	Val	Gly	Val	Ser	Glu	Glu	Thr	Thr	Thr	Gly	Val
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Lys	Arg	Ser	Tyr	Gln	Met	Gln	Pro	Lys	Cys	Thr	Leu	Leu	Leu	His	Ala
			180					185					190		
Thr	Asp	Val	Cys	Asp	Thr	Val	Ile	Lys	Ser	Lys	Ile	Asp	Asn	Leu	Tyr
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Arg	Arg	Pro	Cys	Lys	Val	Ala	Leu	Val	Gly	Gly	Tyr	Gly	Asp	Val	Phe
225					230					235					240
Lys	Gly	Trp	Val	Ala	Ala	Leu	Lys	Gln	Ala	Gly	Ala	Arg	Val	Ile	Val
				245					250					255	
Thr	Glu	Ile	Pro	Gln	Ile	Cys	Ala	Val	Gln	Ala	Thr	Met	Glu	Gly	Ser
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Ser	Val	Leu	Thr	Leu	Glu	Asp	Val	Val	Ser	Asp	Val	Asp	Arg	Phe	Val
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Met	Lys	Asn	Gln	Ala	Ile	Val	Cys	Asn	Ile	Arg	Arg	Phe	Asp	Asn	Glu
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Ile	Asp	Met	Arg	Ser	Leu	Glu	Thr	Phe	Pro	Gly	Val	Lys	Arg	Ile	Thr
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Ile	Lys	Ala	Gln	Thr	Asp	Arg	Trp	Val	Phe	Arg	Asp	Thr	Asn	Arg	Gly
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Ile	Ile	Val	Pro	Ala	Glu	Gly	Arg	Leu	Met	Thr	Met	Gly	Cys	Ala	Thr
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	370					375					380				
Ser	Gln	Leu	Glu	Leu	Trp	Arg	Glu	Lys	Ser	Thr	Gly	Lys	Tyr	Glu	Lys
385					390					395					400
Lys	Val	Tyr	Val	Phe	Pro	Lys	His	Leu	Glu	Lys	Lys	Val	Ala	Ala	Leu

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His	Leu	Val	Lys	Leu	Gly	Ala	Arg	Leu	Thr	Lys	Leu	Ser	Arg	Cys	Thr				
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Leu	Leu	Cys	Thr	Asp	Asp	Pro	Val	Glu	Gly	Arg	Lys	Glu	Pro	Pro	His				
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Asp	Val	Asp		Ile	Val	Arg	Leu	Arg	Lys	Arg	Phe	Phe	Lys	Leu	Asp	
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aga	gat	tgt	tca	gga	tca	gaa	ctt	gga	agt	gag	ttc	atg	agt	ttg	cct	144
Arg	Asp	Cys	Ser	Gly	Ser	Glu	Leu	Gly	Ser	Glu	Phe	Met	Ser	Leu	Pro	
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caa	gtt	agt	tcg	aac	cct	ctt	cgg	atg	cgt	gag	atg	cgt	aat	ttc	gat	192
Gln	Val	Ser	Ser	Asn	Pro	Leu	Arg	Met	Arg	Glu	Met	Arg	Asn	Phe	Asp	
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Asn	Asp	Cys	Val	Gly	Ser	Val	Asp	Phe	Ile	Glu	Phe	Ile	Asn	Gly	Arg	
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tcc	agt	ttc	agt	act	gtc	ggg	cag	aag	aat	gct	aaa	ttg	aga	ttt	gca	288
Ser	Ser	Phe	Ser	Thr	Val	Gly	Gln	Lys	Asn	Ala	Lys	Leu	Arg	Phe	Ala	
				85					90					95		
ccg	att	atc	tat	gat	tgc	gat	aaa	gat	gga	cct	ata	tca	aac	ggg	gag	336
Pro	Ile	Ile	Tyr	Asp	Cys	Asp	Lys	Asp	Gly	Pro	Ile	Ser	Asn	Gly	Glu	
			100					105					110			
tta	ttt	agg	gtg	ttg	cgt	att	atg	gtt	cat	gac	aat	ctg	agt	gat	aat	384
Leu	Phe	Arg	Val	Leu	Arg	Ile	Met	Val	His	Asp	Asn	Leu	Ser	Asp	Asn	
			115				120					125				
cag	ctg	cag	cag	cgt	tgc	gat	tgc	acg	cgt	agt	ggc	gga	gat	aat	gac	432
Gln	Leu	Gln	Gln	Arg	Cys	Asp	Cys	Thr	Arg	Ser	Gly	Gly	Asp	Asn	Asp	

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 145 150 155 160
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 165 170 175
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 Asp Val
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 ttttaggctt ttagagaaaa aggctaaaaa aaaggctaga aaaaaaggct cttaggcctg 697
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 35 40 45
 Gln Val Ser Ser Asn Pro Leu Arg Met Arg Glu Met Arg Asn Phe Asp
 50 55 60
 Asn Asp Cys Val Gly Ser Val Asp Phe Ile Glu Phe Ile Asn Gly Arg
 65 70 75 80
 Ser Ser Phe Ser Thr Val Gly Gln Lys Asn Ala Lys Leu Arg Phe Ala
 85 90 95
 Pro Ile Ile Tyr Asp Cys Asp Lys Asp Gly Pro Ile Ser Asn Gly Glu
 100 105 110
 Leu Phe Arg Val Leu Arg Ile Met Val His Asp Asn Leu Ser Asp Asn
 115 120 125
 Gln Leu Gln Gln Arg Cys Asp Cys Thr Arg Ser Gly Gly Asp Asn Asp
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 Trp Ala Val Asn Pro Cys Phe Ile Ala Ser Cys Ser Cys Leu Leu Val
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 Gly Phe Gly Asp Ala Ile Phe Tyr Glu Ser Phe Ala Gly Asp Phe Asp
 35 40 45

gca cgc tgg att tta tcc ggc tca aag tgt ctc tcg gat tcg gcc aag 195
 Ala Arg Trp Ile Leu Ser Gly Ser Lys Cys Leu Ser Asp Ser Ala Lys
 50 55 60

aat gct ggg ttt gat gat tat gga ctt ctt gtg ggt gaa caa gcc agg 243
 Asn Ala Gly Phe Asp Asp Tyr Gly Leu Leu Val Gly Glu Gln Ala Arg
 65 70 75

aag cct cct ata gtc aag gaa ctt gcc gag tct ctc agt cta aag gac 291
 Lys Pro Pro Ile Val Lys Glu Leu Ala Glu Ser Leu Ser Leu Lys Asp
 80 85 90

gga aga gtt gtt ctt gag tgt gag act cgc ctt gac cat ggc atc gac 339
 Gly Arg Val Val Leu Glu Cys Glu Thr Arg Leu Asp His Gly Ile Asp
 95 100 105 110

tgt gga ggt ccc tgt att aga tat ctt cga acc cag gag agc gga tgg 387
 Cys Gly Gly Pro Cys Ile Arg Tyr Leu Arg Thr Gln Glu Ser Gly Trp
 115 120 125

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 Lys Phe Asp Ser Ser Thr Met Phe Gly Ala Ala Lys Tyr Gly Ala Arg
 130 135 140

agg acc cag ttc ttc ggg ggc cac ccc cag aac cca aac agt ggt gag 483
 Arg Thr Gln Phe Phe Gly Gly His Pro Gln Asn Pro Asn Ser Gly Glu
 145 150 155

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Cys Val Asp His Asp His Asn Gln Arg Ala Ser Leu Thr Ser Asp Lys	
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gta cct cgt ttg tac act gga att ctg tcg ccc gaa aat gaa ttc cag	579
Val Pro Arg Leu Tyr Thr Gly Ile Leu Ser Pro Glu Asn Glu Phe Gln	
175 180 185 190	
atc ttg ata gat cgg ggg ttg gag acc aag gcc aaa atc ttc cct tgt	627
Ile Leu Ile Asp Arg Gly Leu Glu Thr Lys Ala Lys Ile Phe Pro Cys	
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Glu Asp Phe Glu Pro Pro Val Ile Pro Ser Lys Arg Ser Pro Asp Asn	
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Pro Ser Lys Arg Thr Glu Asp Ser Asp Glu Lys Ala Lys Ile Pro Gly	
225 230 235	
cca agt gcc ctg aag cga cag gaa agc gat gag gat ccg aac cgg gaa	771
Pro Ser Ala Leu Lys Arg Gln Glu Ser Asp Glu Asp Pro Asn Arg Glu	
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atc tta cat gaa gaa gcc ggg aga cgt tcg tcc gat gtt ggg gcc cac	819
Ile Leu His Glu Glu Ala Gly Arg Arg Ser Ser Asp Val Gly Ala His	
255 260 265 270	
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Ala Lys Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu	
275 280 285	
aag gat ggt gaa tgc gca ccc cca aag att gaa aac gca aag cgg ggg	915
Lys Asp Gly Glu Cys Ala Pro Pro Lys Ile Glu Asn Ala Lys Arg Gly	
290 295 300	
gcc gcc cct agt tgt ggt gta tcg gag agg caa acc aag att agt cca	963
Ala Ala Pro Ser Cys Gly Val Ser Glu Arg Gln Thr Lys Ile Ser Pro	
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aat tat aag gga aaa ccc tcc gtg ggt cca aac gtt tac caa ggg att	1011
Asn Tyr Lys Gly Lys Pro Ser Val Gly Pro Asn Val Tyr Gln Gly Ile	
320 325 330	
tgg aaa ccc cgc gag atg cta aac cct gga tcg ttc caa atc gca aaa	1059
Trp Lys Pro Arg Glu Met Leu Asn Pro Gly Ser Phe Gln Ile Ala Lys	
335 340 345 350	
ccc gct tgt gag cct att gct ggt ata ggc atg gag att agg aag cag	1107
Pro Ala Cys Glu Pro Ile Ala Gly Ile Gly Met Glu Ile Arg Lys Gln	
355 360 365	
ggc atc cta tta gac act gtg gtg ggg gtt agg ggg gat aca ggt gaa	1155
Gly Ile Leu Leu Asp Thr Val Val Gly Val Arg Gly Asp Thr Gly Glu	
370 375 380	

gaa tat ggg gaa acc ccg ttg aag acc acg tgt acc gtc gag aag cac 1203
 Glu Tyr Gly Glu Thr Pro Leu Lys Thr Thr Cys Thr Val Glu Lys His
 385 390 395

agt ttg cag gct caa gag gcg aga acc cgg tca gac gct ggt tca ccc 1251
 Ser Leu Gln Ala Gln Glu Ala Arg Thr Arg Ser Asp Ala Gly Ser Pro
 400 405 410

tac acc agg tac gta tct aaa atc ccc ggg aaa gcc gat aat ccc ttc 1299
 Tyr Thr Arg Tyr Val Ser Lys Ile Pro Gly Lys Ala Asp Asn Pro Phe
 415 420 425 430

tcg agc gag cac aaa tgt aag aat ttc gat ctg att gag gct gag aaa 1347
 Ser Ser Glu His Lys Cys Lys Asn Phe Asp Leu Ile Glu Ala Glu Lys
 435 440 445

cag tgt gcc aat gca gta atc ctg ggt gtt gtg gtt aac tcc ggt tca 1395
 Gln Cys Ala Asn Ala Val Ile Leu Gly Val Val Val Asn Ser Gly Ser
 450 455 460

att aac tcc gtt gtg tct tgg ggc tac aaa cct ggc acg gtg aac aag 1443
 Ile Asn Ser Val Val Ser Trp Gly Tyr Lys Pro Gly Thr Val Asn Lys
 465 470 475

aac caa gaa cgc aga gca ccc tcc cag cga cgt agt agc gag att gaa 1491
 Asn Gln Glu Arg Arg Ala Pro Ser Gln Arg Arg Ser Ser Glu Ile Glu
 480 485 490

gga acc caa gac cga cga aaa cag gat gtt ggc cga cgc caa gct gcc 1539
 Gly Thr Gln Asp Arg Arg Lys Gln Asp Val Gly Arg Arg Gln Ala Ala
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 35 40 45

Trp Ile Leu Ser Gly Ser Lys Cys Leu Ser Asp Ser Ala Lys Asn Ala
 50 55 60

Gly Phe Asp Asp Tyr Gly Leu Leu Val Gly Glu Gln Ala Arg Lys Pro
 65 70 75 80
 Pro Ile Val Lys Glu Leu Ala Glu Ser Leu Ser Leu Lys Asp Gly Arg
 85 90 95
 Val Val Leu Glu Cys Glu Thr Arg Leu Asp His Gly Ile Asp Cys Gly
 100 105 110
 Gly Pro Cys Ile Arg Tyr Leu Arg Thr Gln Glu Ser Gly Trp Lys Phe
 115 120 125
 Asp Ser Ser Thr Met Phe Gly Ala Ala Lys Tyr Gly Ala Arg Arg Thr
 130 135 140
 Gln Phe Phe Gly Gly His Pro Gln Asn Pro Asn Ser Gly Glu Cys Val
 145 150 155 160
 Asp His Asp His Asn Gln Arg Ala Ser Leu Thr Ser Asp Lys Val Pro
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 Arg Leu Tyr Thr Gly Ile Leu Ser Pro Glu Asn Glu Phe Gln Ile Leu
 180 185 190
 Ile Asp Arg Gly Leu Glu Thr Lys Ala Lys Ile Phe Pro Cys Glu Asp
 195 200 205
 Phe Glu Pro Pro Val Ile Pro Ser Lys Arg Ser Pro Asp Asn Pro Ser
 210 215 220
 Lys Arg Thr Glu Asp Ser Asp Glu Lys Ala Lys Ile Pro Gly Pro Ser
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 Ala Leu Lys Arg Gln Glu Ser Asp Glu Asp Pro Asn Arg Glu Ile Leu
 245 250 255
 His Glu Glu Ala Gly Arg Arg Ser Ser Asp Val Gly Ala His Ala Lys
 260 265 270
 Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu Lys Asp
 275 280 285
 Gly Glu Cys Ala Pro Pro Lys Ile Glu Asn Ala Lys Arg Gly Ala Ala
 290 295 300
 Pro Ser Cys Gly Val Ser Glu Arg Gln Thr Lys Ile Ser Pro Asn Tyr
 305 310 315 320
 Lys Gly Lys Pro Ser Val Gly Pro Asn Val Tyr Gln Gly Ile Trp Lys
 325 330 335
 Pro Arg Glu Met Leu Asn Pro Gly Ser Phe Gln Ile Ala Lys Pro Ala
 340 345 350
 Cys Glu Pro Ile Ala Gly Ile Gly Met Glu Ile Arg Lys Gln Gly Ile
 355 360 365

Leu Leu Asp Thr Val Val Gly Val Arg Gly Asp Thr Gly Glu Glu Tyr
370 375 380

Gly Glu Thr Pro Leu Lys Thr Thr Cys Thr Val Glu Lys His Ser Leu
385 390 395 400

Gln Ala Gln Glu Ala Arg Thr Arg Ser Asp Ala Gly Ser Pro Tyr Thr
405 410 415

Arg Tyr Val Ser Lys Ile Pro Gly Lys Ala Asp Asn Pro Phe Ser Ser
420 425 430

Glu His Lys Cys Lys Asn Phe Asp Leu Ile Glu Ala Glu Lys Gln Cys
435 440 445

Ala Asn Ala Val Ile Leu Gly Val Val Val Asn Ser Gly Ser Ile Asn
450 455 460

Ser Val Val Ser Trp Gly Tyr Lys Pro Gly Thr Val Asn Lys Asn Gln
465 470 475 480

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Pro Arg Arg
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Arg Val Thr Arg Asp Gly Ser Gly Pro Gly Lys Thr Gly Val Thr Arg
15 20 25

ggg tcg tca ccc atg cga tgg gca tgg aag cgg tgg caa gcc gtc ggg 147
Gly Ser Ser Pro Met Arg Trp Ala Trp Lys Arg Trp Gln Ala Val Gly
30 35 40 45

gca tcg acg gcc cgc acg tgg ttc ggg aca gag aac cag aaa gga ata 195
Ala Ser Thr Ala Arg Thr Trp Phe Gly Thr Glu Asn Gln Lys Gly Ile
50 55 60

acg aca agc acc cgc gcg cgg cgc tac gcg gtc tcg gcc aaa ttc ccg	243
Thr Thr Ser Thr Arg Ala Arg Arg Tyr Ala Val Ser Ala Lys Phe Pro	
65 70 75	
aga tta agt aat aag ggc aaa gat tac atg cgt tgc gtc ctc caa tac	291
Arg Leu Ser Asn Lys Gly Lys Asp Tyr Met Arg Cys Val Leu Gln Tyr	
80 85 90	
acc gtc aaa aat gaa caa aaa gtt gat tgt ggt ggc tca tat atc aag	339
Thr Val Lys Asn Glu Gln Lys Val Asp Cys Gly Gly Ser Tyr Ile Lys	
95 100 105	
tta tta cct tcg aaa ttg cgc acg ggt gat ggt gat ggc gtg tca gaa	387
Leu Leu Pro Ser Lys Leu Arg Thr Gly Asp Gly Asp Gly Val Ser Glu	
110 115 120 125	
tat tca att atg ttt ggt cca gat tcg aca ggt gca tca cgt act gtt	435
Tyr Ser Ile Met Phe Gly Pro Asp Ser Thr Gly Ala Ser Arg Thr Val	
130 135 140	
cgt cga gct cgc aat tat aag ggt aaa cgg cat ttg cgg aaa aaa gaa	483
Arg Arg Ala Arg Asn Tyr Lys Gly Lys Arg His Leu Arg Lys Lys Glu	
145 150 155	
cag aat aaa gtg gaa aca gat caa tta aca cat cag tat act acg agt	531
Gln Asn Lys Val Glu Thr Asp Gln Leu Thr His Gln Tyr Thr Thr Ser	
160 165 170	
tgg tca cca gat tgg acc tac aac gtt cta gta gat aat aag gaa tcg	579
Trp Ser Pro Asp Trp Thr Tyr Asn Val Leu Val Asp Asn Lys Glu Ser	
175 180 185	
caa gca ggg aac ctt gcc gac gac tgc gag tta ctt cca cag aag cga	627
Gln Ala Gly Asn Leu Ala Asp Asp Cys Glu Leu Leu Pro Gln Lys Arg	
190 195 200 205	
atc ttc cga ccc agc tgc cga aaa caa tcc aaa cca gtc acc tgc gta	675
Ile Phe Arg Pro Ser Cys Arg Lys Gln Ser Lys Pro Val Thr Cys Val	
210 215 220	
gac gtc aag cac cac gcc ccc cga cga aat gtg aaa ccc gcc ggg cac	723
Asp Val Lys His His Ala Pro Arg Arg Asn Val Lys Pro Ala Gly His	
225 230 235	
gat gac att cca gcg cga cgg acg acg ccg gaa gcg gtc cgg aaa ggc	771
Asp Asp Ile Pro Ala Arg Arg Thr Thr Pro Glu Ala Val Arg Lys Gly	
240 245 250	
cgc acg aac gag cga ccg gac cgg acg tgg gcg acc ggg acg acc cca	819
Arg Thr Asn Glu Arg Pro Asp Arg Thr Trp Ala Thr Gly Thr Thr Pro	
255 260 265	
cgg cca cgg cgt tac aag gga gag acg aag gcc aaa aag cac cca cgg	867
Arg Pro Arg Arg Tyr Lys Gly Glu Thr Lys Ala Lys Lys His Pro Arg	
270 275 280 285	

ccg gaa tac aaa ggg acc tgg gtc acg ccg tta cag gac aac ccc act 915
 Pro Glu Tyr Lys Gly Thr Trp Val Thr Pro Leu Gln Asp Asn Pro Thr
 290 295 300

cca gcc ccc ccg aac gac cta tat cta ttc ttg gac ctg ggt gca gca 963
 Pro Ala Pro Pro Asn Asp Leu Tyr Leu Phe Leu Asp Leu Gly Ala Ala
 305 310 315

ggg aca cgg acc tgg acc gtg aaa tcg ggc tca atc acg aac aac atg 1011
 Gly Thr Arg Thr Trp Thr Val Lys Ser Gly Ser Ile Thr Asn Asn Met
 320 325 330

ata gtg aca acg tcc gtg gaa acc gcg acc gac ttc tca gag aaa acc 1059
 Ile Val Thr Thr Ser Val Glu Thr Ala Thr Asp Phe Ser Glu Lys Thr
 335 340 345

aag gtg gca aac acc acg acc gag ctc aac gac gga cgc gac gcc gga 1107
 Lys Val Ala Asn Thr Thr Thr Glu Leu Asn Asp Gly Arg Asp Ala Gly
 350 355 360 365

acg ggg atc ggt gcc gag cgc cac tgt gct gat gag aga tgg aaa gag 1155
 Thr Gly Ile Gly Ala Glu Arg His Cys Ala Asp Glu Arg Trp Lys Glu
 370 375 380

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 Thr Thr Val Ala Pro Asp Cys Ala Val Ser Ala Ala Asn Ala Ser Arg
 385 390 395

cgc acc ggg gag ctg gcc acc ccg gtg acg atg ctg cct gat ccg ttg 1251
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 35 40 45

Ala Arg Thr Trp Phe Gly Thr Glu Asn Gln Lys Gly Ile Thr Thr Ser
 50 55 60

Thr Arg Ala Arg Arg Tyr Ala Val Ser Ala Lys Phe Pro Arg Leu Ser
 65 70 75 80

Asn Lys Gly Lys Asp Tyr Met Arg Cys Val Leu Gln Tyr Thr Val Lys
 85 90 95
 Asn Glu Gln Lys Val Asp Cys Gly Gly Ser Tyr Ile Lys Leu Leu Pro
 100 105 110
 Ser Lys Leu Arg Thr Gly Asp Gly Asp Gly Val Ser Glu Tyr Ser Ile
 115 120 125
 Met Phe Gly Pro Asp Ser Thr Gly Ala Ser Arg Thr Val Arg Arg Ala
 130 135 140
 Arg Asn Tyr Lys Gly Lys Arg His Leu Arg Lys Lys Glu Gln Asn Lys
 145 150 155 160
 Val Glu Thr Asp Gln Leu Thr His Gln Tyr Thr Thr Ser Trp Ser Pro
 165 170 175
 Asp Trp Thr Tyr Asn Val Leu Val Asp Asn Lys Glu Ser Gln Ala Gly
 180 185 190
 Asn Leu Ala Asp Asp Cys Glu Leu Leu Pro Gln Lys Arg Ile Phe Arg
 195 200 205
 Pro Ser Cys Arg Lys Gln Ser Lys Pro Val Thr Cys Val Asp Val Lys
 210 215 220
 His His Ala Pro Arg Arg Asn Val Lys Pro Ala Gly His Asp Asp Ile
 225 230 235 240
 Pro Ala Arg Arg Thr Thr Pro Glu Ala Val Arg Lys Gly Arg Thr Asn
 245 250 255
 Glu Arg Pro Asp Arg Thr Trp Ala Thr Gly Thr Thr Pro Arg Pro Arg
 260 265 270
 Arg Tyr Lys Gly Glu Thr Lys Ala Lys Lys His Pro Arg Pro Glu Tyr
 275 280 285
 Lys Gly Thr Trp Val Thr Pro Leu Gln Asp Asn Pro Thr Pro Ala Pro
 290 295 300
 Pro Asn Asp Leu Tyr Leu Phe Leu Asp Leu Gly Ala Ala Gly Thr Arg
 305 310 315 320
 Thr Trp Thr Val Lys Ser Gly Ser Ile Thr Asn Asn Met Ile Val Thr
 325 330 335
 Thr Ser Val Glu Thr Ala Thr Asp Phe Ser Glu Lys Thr Lys Val Ala
 340 345 350
 Asn Thr Thr Thr Glu Leu Asn Asp Gly Arg Asp Ala Gly Thr Gly Ile
 355 360 365
 Gly Ala Glu Arg His Cys Ala Asp Glu Arg Trp Lys Glu Thr Thr Val
 370 375 380

Ala Pro Asp Cys Ala Val Ser Ala Ala Asn Ala Ser Arg Arg Thr Gly
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aca aaa gag ctg gga aca gtt atg cgt tca cta gga caa aac cca aca 96
Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr
20 25 30

gag gct gag ctc caa gac atg atc aac gag gtt gat gca gat gga aac 144
Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn
35 40 45

ggc act atc gac ttc ccc gag ttc ctg aac ctg atg gct aag aag atg 192
Gly Thr Ile Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Lys Lys Met
50 55 60

aaa gac act gac tcc gag gaa gag cta aaa gaa gcc ttc agg gtt ttc 240
Lys Asp Thr Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe
65 70 75 80

gac aaa gac cag aac ggt ttc atc tcc gct gct gag cta cgc cat gtg 288
Asp Lys Asp Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val
85 90 95

atg acc aat ctt ggt gag aag cta act gat gaa gaa gtg gaa gag atg 336
Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Glu Glu Met
100 105 110

atc cgt gag gct gat gtt gat gga gat ggt cag att aac tat gaa gag 384
Ile Arg Glu Ala Asp Val Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu
115 120 125

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Phe Val Lys Ile Met Met Ala Lys
130 135

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 35 40 45
 Gly Thr Ile Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Lys Lys Met
 50 55 60
 Lys Asp Thr Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe
 65 70 75 80
 Asp Lys Asp Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val
 85 90 95
 Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Glu Glu Met
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 Ile Arg Glu Ala Asp Val Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu
 115 120 125
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 Asn Ser Ser Leu Ser Ser Gly Asn Gly Thr Glu Val Ala Thr Asp Val
 10 15 20

tct tct tgc ttc tat gtt ccc aat ccc tct gga acc gat ttc gat gcc 150
 Ser Ser Cys Phe Tyr Val Pro Asn Pro Ser Gly Thr Asp Phe Asp Ala
 25 30 35

gag tcg tct tct ctt cct cct ct gtaagtcttc ttggaatttt taaaaacatt 203
 Glu Ser Ser Ser Leu Pro Pro Le
 40 45

cactctcttg ctgctgtctc tgttgatcct tcttctttga aaatttgaaa acattcttag 263

tctctcgctc tgtcacag c tcc cca gct cct caa gtg gca ttg tca att cct 315
 u Ser Pro Ala Pro Gln Val Ala Leu Ser Ile Pro
 50 55

gcg gag ctt gcc gcc gcc att ccc ctc atc gat cgc ttc cag gtt gaa 363
 Ala Glu Leu Ala Ala Ala Ile Pro Leu Ile Asp Arg Phe Gln Val Glu
 60 65 70

gct ttt ctg cgg cta atg cag aaa caa atc cag tct gct ggg aag cgt 411
 Ala Phe Leu Arg Leu Met Gln Lys Gln Ile Gln Ser Ala Gly Lys Arg
 75 80 85 90

ggc ttc ttc tat tcc aaa aag tcc tct ggc tcc aat gtc cgc gag cgc 459
 Gly Phe Phe Tyr Ser Lys Lys Ser Ser Gly Ser Asn Val Arg Glu Arg
 95 100 105

ttc aca ttt gag gat atg ctt tgc ttt caa aag gtttttcttt ccccccttt 512
 Phe Thr Phe Glu Asp Met Leu Cys Phe Gln Lys
 110 115

cttccccatt gacaatccat tgactg aat atg tct ctc tcc cct tcc ttc ctt 565
 Asn Met Ser Leu Ser Pro Ser Phe Leu
 120 125

cag gat cca atc ccc aca tct ctc ctc aag att aac agc gat ctc gtc 613
 Gln Asp Pro Ile Pro Thr Ser Leu Leu Lys Ile Asn Ser Asp Leu Val
 130 135 140

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agc cgt gct acc aag ttg ttt cat ctc atc tta aaa tat atg ggt gtt 661
Ser Arg Ala Thr Lys Leu Phe His Leu Ile Leu Lys Tyr Met Gly Val
      145                150                155

gat tca tct gat cga tct acg cct ccc agt tta gat gaa cgc att gac 709
Asp Ser Ser Asp Arg Ser Thr Pro Pro Ser Leu Asp Glu Arg Ile Asp
      160                165                170

ctc gtt gga aag ctc ttc aaa aaa act ttg aag cgt gtt gaa ctc agg 757
Leu Val Gly Lys Leu Phe Lys Lys Thr Leu Lys Arg Val Glu Leu Arg
      175                180                185                190

gac gaa ctt ttt gcc caa atc tcc aaa cag act aga cat aat cct gac 805
Asp Glu Leu Phe Ala Gln Ile Ser Lys Gln Thr Arg His Asn Pro Asp
      195                200                205

agg caa tac ttg atc aaa gct tgg gaa ttg atg tac tta tgt gcc tcc 853
Arg Gln Tyr Leu Ile Lys Ala Trp Glu Leu Met Tyr Leu Cys Ala Ser
      210                215                220

tct atg cct cct agc aaa gat atc ggt gga tat cta tct gag tat att 901
Ser Met Pro Pro Ser Lys Asp Ile Gly Gly Tyr Leu Ser Glu Tyr Ile
      225                230                235

cat aat gtc gca cac gat gca act att gaa ccg gat gct cag gtt ctt 949
His Asn Val Ala His Asp Ala Thr Ile Glu Pro Asp Ala Gln Val Leu
      240                245                250

gct gtt aac act ttg aaa gct tta aag cgc tct atc aaa gct ggt cct 997
Ala Val Asn Thr Leu Lys Ala Leu Lys Arg Ser Ile Lys Ala Gly Pro
      255                260                265                270

agg cac acc aca cct ggt cgt gaa gaa att gaa gcc ctt ttg acc ggt 1045
Arg His Thr Thr Pro Gly Arg Glu Glu Ile Glu Ala Leu Leu Thr Gly
      275                280                285

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Arg Lys Leu Thr Thr Ile Val Phe Phe Leu Asp Glu Thr Phe Glu Glu
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Ile Ser Tyr Asp Met Ala Thr Thr Val Ser Asp Ala Val Glu
      305                310                315

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ctcactgcat tgacatctgt ttcaggag cta gct gga aca att aaa cta tca 1247
Leu Ala Gly Thr Ile Lys Leu Ser
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gct ttc tct agc ttt agt ttg ttt gaa tgt cgt aaa gtt gtt tca agt 1295
Ala Phe Ser Ser Phe Ser Leu Phe Glu Cys Arg Lys Val Val Ser Ser
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Ser Lys Ser Ser Asp Pro Gly Asn G

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345

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 lu Glu Tyr Ile Gly Leu Asp Asp Asn Lys Tyr Ile Gly Asp Leu
 350 355 360
 ctc gca gaa ttt aaa gct att aaa gac cga aat aaa gga gag ata cta 1495
 Leu Ala Glu Phe Lys Ala Ile Lys Asp Arg Asn Lys Gly Glu Ile Leu
 365 370 375
 cac tgc aaa ctg gta ttt aaa aaa aaa tta ttc cga gag tct gat gaa 1543
 His Cys Lys Leu Val Phe Lys Lys Lys Leu Phe Arg Glu Ser Asp Glu
 380 385 390 395
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 Ala Val Thr Asp Leu Met Phe Val Gln Leu Ser Tyr Val Gln
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 Leu Gln His Asp Tyr Leu Leu Gly Asn Tyr Pro
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 Val Gly Arg Asp Asp Ala Ala Gln Leu Cys Ala Leu Gln Ile Leu Val
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 Gly Ile Gly Phe Val Asn Ser Pro Glu Ser Cys Il
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 e Asp Trp Thr Ser
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 Arg Glu Trp Glu Leu Asp Ile Leu Ala Arg Tyr Arg Ser Met
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 Glu Asn Val Thr Lys Asp Asp Ala Arg Gln Gln Phe Leu Arg Ile Leu
 485 490 495
 aag gca ctg cca tac ggg aat tca gtt ttt ttt agc gta cgc aag ata 2209

125

Lys Ala Leu Pro Tyr Gly Asn Ser Val Phe Phe Ser Val Arg Lys Ile
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 Asp Asp Pro Ile Gly Leu Leu Pro Gly Arg Ile Ile Leu Gly Ile Asn
 515 520 525 530

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 Lys Arg Gly

aactgttatt gttgtttgga attcaaatct atgttggttg atttgaattt gttgtttgct 2366

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 Val His Phe Phe Arg Pro Val Pro Lys Glu Tyr Leu His Ser
 535 540 545

gct gaa cta cgt gac atc atg caa ttt ggc agc agt aac act gct gtc 2465
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 550 555 560

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 565 570 575

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 Thr Lys Gln
 580

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 Gly Glu Glu Ile
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 590 595 600

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 Ser Lys Ala Arg Ser Ala Ala Asn Cys Leu Val Asn Gly Asp Ile Ser
 605 610 615

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 Asp Leu Ser Lys Ala Tyr Glu Glu Ser Gln Lys Lys Ile Glu Lys
 635 640 645

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atgtagaatg ttataccatg acctcttttg ttttagagtg gcatgctgat gaactattcg 3048

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Leu Met Asp Glu Gln Gln Glu Lys Asn Gln
 650 655

caa gaa gtt act ctg cgt gaa gag tta gaa gct ata cac aat ggt ttg 3148
 Gln Glu Val Thr Leu Arg Glu Glu Leu Glu Ala Ile His Asn Gly Leu
 660 665 670 675

gag ctt gaa agg aga aaa ttg ttg gag gtt act tta gac cga gat aaa 3196
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 680 685 690

ctt agg tca ttg tgt gac gag aag gga acc cct att caa gttagttata 3245
 Leu Arg Ser Leu Cys Asp Glu Lys Gly Thr Pro Ile Gln
 695 700

acctaacttt tgtctttctt ttgatgcttg gttgaagtta tttaatgatt tattctatat 3305

atgctatag tcc ttg atg tct gaa ctg cga gga atg gaa gca agg ttg gca 3356
 Ser Leu Met Ser Glu Leu Arg Gly Met Glu Ala Arg Leu Ala
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 Lys Ser Gly Asn Thr Lys Ser Ser Lys Glu Thr Lys Ser Glu Leu Ala
 720 725 730

gaa atg aat aat cag gtgaatatta tgtgtttaaa tctaattcat tgtaatcatt 3459
 Glu Met Asn Asn Gln
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 Ile Leu Tyr Lys Ile Gln Lys Glu Leu Glu Val Arg Asn Lys Glu Leu
 740 745 750 755

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 His Val Ala Val Asp Asn Ser Lys Arg Leu Leu Ser Glu Asn Lys Ile
 760 765 770

ttg gag caa aat ctc aat att gaa aag aag aaa aaa gag gag 3656
 Leu Glu Gln Asn Leu Asn Ile Glu Lys Lys Lys Lys Glu Glu
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ata aca cgt gta tca tgc gca atc ggg aga ttc cct tat gct tgt aat	1440
Ile Thr Arg Val Ser Cys Ala Ile Gly Arg Phe Pro Tyr Ala Cys Asn	
465 470 475 480	
tac cca caa cag ctc cca caa gca tca caa cac cag cta cag caa cag	1488
Tyr Pro Gln Gln Leu Pro Gln Ala Ser Gln His Gln Leu Gln Gln Gln	
485 490 495	
caa caa aaa cga ccg gcg tta caa cca aag caa gaa caa ccg gaa gta	1536
Gln Gln Lys Arg Pro Ala Leu Gln Pro Lys Gln Glu Gln Pro Glu Val	
500 505 510	
gag aaa cac cga tta caa ata cca cgt caa aat tta gct gta tat aat	1584
Glu Lys His Arg Leu Gln Ile Pro Arg Gln Asn Leu Ala Val Tyr Asn	
515 520 525	
agt aat cac gat ata tgg aat aat cgc aat aga gat aaa tat att att	1632
Ser Asn His Asp Ile Trp Asn Asn Arg Asn Arg Asp Lys Tyr Ile Ile	
530 535 540	
agt aac aat cct aat aat agg aat gat aat aat aac act gta tgc gat	1680
Ser Asn Asn Pro Asn Asn Arg Asn Asp Asn Asn Asn Thr Val Cys Asp	
545 550 555 560	
cta agc agt ggc gag tta ggt gaa agt cgt gag gtt gtg cca gac ggt	1728
Leu Ser Ser Gly Glu Leu Gly Glu Ser Arg Glu Val Val Pro Asp Gly	
565 570 575	
atc ggg ttg gag gta ctt cta gat tct atc gta aaa gaa gag gta cga	1776
Ile Gly Leu Glu Val Leu Leu Asp Ser Ile Val Lys Glu Glu Val Arg	
580 585 590	
atg gaa cca tca aca gtt tcg aag gaa ttt agg tcg atc att tct gaa	1824
Met Glu Pro Ser Thr Val Ser Lys Glu Phe Arg Ser Ile Ile Ser Glu	
595 600 605	
tgt tta cga aac gat gca act gaa aga caa aca gct tca aac tta gta	1872
Cys Leu Arg Asn Asp Ala Thr Glu Arg Gln Thr Ala Ser Asn Leu Val	

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aat cac gaa ttt gta aag aaa tat caa aag tac aat cgt gaa aaa tgg      1920
Asn His Glu Phe Val Lys Lys Tyr Gln Lys Tyr Asn Arg Glu Lys Trp
625                630                635                640

acc gca gat tta caa agg tgg caa taa aaatcgctt cagcgctgat      1967
Thr Ala Asp Leu Gln Arg Trp Gln
        645

cgctgacgct cgacgcctgc cccagcctg cagctcgccc agctcgccca ggctcgccca 2027
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Asn Asn Asn Pro Lys Ser His Asn Ser His Asn Ser Asn Gly Met Thr
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Gly Asn Arg Asn Asn Asn Asn Lys Asn Ala Gly Gly Val Glu Thr Ser
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Lys Lys Ala Arg Ser Arg Leu Glu Thr His Pro Arg Asp Asn Glu Asn
  65                70                75                80

Asn Tyr Arg Leu Ala Thr Ser Ala Gly Thr Lys Gly Gly Ala Arg Thr
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Val Asp Val Pro Val Ile Leu Ser Thr Arg Glu Ser Gln Gly Thr Arg
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Ser Val Asn Ala Thr Ser Lys Ile Arg Cys Pro Asp Ser Thr Ala Ile
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Cys Glu Trp Phe Ala Thr Pro Thr Asp Pro Gln Arg Pro Gly Val Tyr
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Asn His Lys Asn Gly Asp Lys Asn Asn Arg Asp Thr Gly Asn Ile Asn
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Thr Val Ser Ser Leu Met Asp Asn Ala Arg Gly Pro Asn Pro Arg Ser
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Gly Ile Ser Ile Pro Thr Pro Thr Ser Arg Gln Ser Pro Ser Glu Thr

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139

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Ser	Asn	His	Asp	Ile	Trp	Asn	Asn	Arg	Asn	Arg	Asp	Lys	Tyr	Ile	Ile						
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545					550				555						560						
Leu	Ser	Ser	Gly	Glu	Leu	Gly	Glu	Ser	Arg	Glu	Val	Val	Pro	Asp	Gly						
			565						570					575							
Ile	Gly	Leu	Glu	Val	Leu	Leu	Asp	Ser	Ile	Val	Lys	Glu	Glu	Val	Arg						
			580					585					590								
Met	Glu	Pro	Ser	Thr	Val	Ser	Lys	Glu	Phe	Arg	Ser	Ile	Ile	Ser	Glu						
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Cys	Leu	Arg	Asn	Asp	Ala	Thr	Glu	Arg	Gln	Thr	Ala	Ser	Asn	Leu	Val						
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Asn	His	Glu	Phe	Val	Lys	Lys	Tyr	Gln	Lys	Tyr	Asn	Arg	Glu	Lys	Trp						
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cga ccg tcg gtt ttc tgt tct att cca ggt ctc ggc ggc gat tcc cac 100
 Arg Pro Ser Val Phe Cys Ser Ile Pro Gly Leu Gly Gly Asp Ser His
 10 15 20 25

cga aaa cct cca agt gac ggt ttc ctc aag ctg cct gcg tcg tct att 148
 Arg Lys Pro Pro Ser Asp Gly Phe Leu Lys Leu Pro Ala Ser Ser Ile
 30 35 40

ccg gcg gac agc cga aaa tta gta gcg aat tct act tcc ttt cat cca 196

Pro	Ala	Asp	Ser	Arg	Lys	Leu	Val	Ala	Asn	Ser	Thr	Ser	Phe	His	Pro		
			45					50					55				
atc	tca	gcc	gtt	aac	gtc	tct	gct	caa	gct	tcc	ctc	acc	gct	gat	ttt	244	
Ile	Ser	Ala	Val	Asn	Val	Ser	Ala	Gln	Ala	Ser	Leu	Thr	Ala	Asp	Phe		
		60					65					70					
ccc	gcc	ctt	tca	gaa	act	ata	ctg	aaa	gag	gga	aga	aat	aac	gga	aaa	292	
Pro	Ala	Leu	Ser	Glu	Thr	Ile	Leu	Lys	Glu	Gly	Arg	Asn	Asn	Gly	Lys		
		75					80				85						
gag	aaa	gca	gag	aac	atc	gtg	tgg	cac	gag	agt	tcg	ata	tgc	aga	tgc	340	
Glu	Lys	Ala	Glu	Asn	Ile	Val	Trp	His	Glu	Ser	Ser	Ile	Cys	Arg	Cys		
	90					95				100					105		
gac	aga	caa	caa	ctt	ctt	caa	caa	aag	ggt	tgt	gtc	gtt	tgg	atc	act	388	
Asp	Arg	Gln	Gln	Leu	Leu	Gln	Gln	Lys	Gly	Cys	Val	Val	Trp	Ile	Thr		
				110					115					120			
ggt	ctc	agt	ggt	tca	ggg	aaa	agc	act	gtt	gct	tgt	gca	cta	agt	aaa	436	
Gly	Leu	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Val	Ala	Cys	Ala	Leu	Ser	Lys		
			125					130					135				
gca	ttg	ttt	gaa	aga	ggc	aaa	ctt	act	tac	aca	ctc	gac	ggc	gac	aat	484	
Ala	Leu	Phe	Glu	Arg	Gly	Lys	Leu	Thr	Tyr	Thr	Leu	Asp	Gly	Asp	Asn		
		140					145					150					
gtc	cgt	cac	ggc	ctt	aac	cgt	gac	ctc	act	ttc	aaa	gca	gag	cac	cgc	532	
Val	Arg	His	Gly	Leu	Asn	Arg	Asp	Leu	Thr	Phe	Lys	Ala	Glu	His	Arg		
	155					160					165						
acc	gaa	aac	att	aga	aga	att	ggt	gag	gtg	gct	aag	ttg	ttt	gct	gac	580	
Thr	Glu	Asn	Ile	Arg	Arg	Ile	Gly	Glu	Val	Ala	Lys	Leu	Phe	Ala	Asp		
	170				175					180					185		
gtc	gga	gtc	att	tgt	ata	gca	agt	ttg	att	tct	ccg	tac	cgg	aga	gac	628	
Val	Gly	Val	Ile	Cys	Ile	Ala	Ser	Leu	Ile	Ser	Pro	Tyr	Arg	Arg	Asp		
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aga	gac	gcg	tgc	cgg	tcc	ttg	tta	cct	gac	ggc	gat	ttc	gtc	gag	gtc	676	
Arg	Asp	Ala	Cys	Arg	Ser	Leu	Leu	Pro	Asp	Gly	Asp	Phe	Val	Glu	Val		
			205					210					215				
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Phe	Met	Asp	Val	Pro	Leu	His	Val	Cys	Glu	Ser	Arg	Asp	Pro	Lys	Gly		
		220					225					230					
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Leu	Tyr	Lys	Leu	Ala	Arg	Ala	Gly	Lys	Ile	Lys	Gly	Phe	Thr	Gly	Ile		
		235				240					245						
gac	gac	cct	tac	gag	gca	cca	gtg	aat	tgc	gag	gta	gtg	ctg	aaa	cac	820	
Asp	Asp	Pro	Tyr	Glu	Ala	Pro	Val	Asn	Cys	Glu	Val	Val	Leu	Lys	His		
		250			255				260						265		
aca	gga	gac	gac	gag	tcg	tgt	tcg	cca	cgt	cag	atg	gct	gag	aac	atc	868	
Thr	Gly	Asp	Asp	Glu	Ser	Cys	Ser	Pro	Arg	Gln	Met	Ala	Glu	Asn	Ile		

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                270                275                280
atc tct tac ctg caa aac aaa ggt tat ctt gag ggc taa gtcaaagtcg      917
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Phe Leu Lys Leu Pro Ala Ser Ser Ile Pro Ala Asp Ser Arg Lys Leu
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Val Ala Asn Ser Thr Ser Phe His Pro Ile Ser Ala Val Asn Val Ser
                50                55                60

Ala Gln Ala Ser Leu Thr Ala Asp Phe Pro Ala Leu Ser Glu Thr Ile
                65                70                75                80

Leu Lys Glu Gly Arg Asn Asn Gly Lys Glu Lys Ala Glu Asn Ile Val
                85                90                95

Trp His Glu Ser Ser Ile Cys Arg Cys Asp Arg Gln Gln Leu Leu Gln
                100                105                110

Gln Lys Gly Cys Val Val Trp Ile Thr Gly Leu Ser Gly Ser Gly Lys
                115                120                125

Ser Thr Val Ala Cys Ala Leu Ser Lys Ala Leu Phe Glu Arg Gly Lys
                130                135                140

Leu Thr Tyr Thr Leu Asp Gly Asp Asn Val Arg His Gly Leu Asn Arg
                145                150                155                160

Asp Leu Thr Phe Lys Ala Glu His Arg Thr Glu Asn Ile Arg Arg Ile
                165                170                175

Gly Glu Val Ala Lys Leu Phe Ala Asp Val Gly Val Ile Cys Ile Ala
                180                185                190

Ser Leu Ile Ser Pro Tyr Arg Arg Asp Arg Asp Ala Cys Arg Ser Leu
                195                200                205

Leu Pro Asp Gly Asp Phe Val Glu Val Phe Met Asp Val Pro Leu His
                210                215                220

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Val Cys Glu Ser Arg Asp Pro Lys Gly Leu Tyr Lys Leu Ala Arg Ala
 225 230 235 240

Gly Lys Ile Lys Gly Phe Thr Gly Ile Asp Asp Pro Tyr Glu Ala Pro
 245 250 255

Val Asn Cys Glu Val Val Leu Lys His Thr Gly Asp Asp Glu Ser Cys
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 275 280 285

Gly Tyr Leu Glu Gly
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 Ser Gly Ala Ser Thr Lys Tyr Asp Ala Lys Asp Ile Gly Ser Leu Gly
 15 20 25

agc aag gct tcg tct gtg tct gta aga cca agc cct cga act gag ggt 147
 Ser Lys Ala Ser Ser Val Ser Val Arg Pro Ser Pro Arg Thr Glu Gly
 30 35 40 45

gag atc tta cag tct cca aat ctc aag agt ttt agc ttt gct gag ctt 195
 Glu Ile Leu Gln Ser Pro Asn Leu Lys Ser Phe Ser Phe Ala Glu Leu
 50 55 60

aaa tca gca acc agg aat ttt aga cca gac agt gtg ctt ggt gaa ggt 243
 Lys Ser Ala Thr Arg Asn Phe Arg Pro Asp Ser Val Leu Gly Glu Gly
 65 70 75

gga ttc ggt tgt gtt ttc aaa gga tgg att gat gag aag tct ctc act 291
 Gly Phe Gly Cys Val Phe Lys Gly Trp Ile Asp Glu Lys Ser Leu Thr
 80 85 90

gcc tca aga cca ggc acg ggt ttg gtt att gcc gtc aaa aag ctt aac 339
 Ala Ser Arg Pro Gly Thr Gly Leu Val Ile Ala Val Lys Lys Leu Asn
 95 100 105

caa gat ggt tgg caa ggt cac cag gag tgg ctg gct gaa gtg aat tac 387
 Gln Asp Gly Trp Gln Gly His Gln Glu Trp Leu Ala Glu Val Asn Tyr

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Leu Gly Gln Phe Ser His Arg His Leu Val Lys Leu Ile Gly Tyr Cys				
130 135 140				
cta gag gat gag cac cgt ctt ctt gtt tac gag ttc atg cct cgg ggt	483			
Leu Glu Asp Glu His Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Gly				
145 150 155				
agc ttg gag aat cat ctt ttc agg aga ggt ttg tac ttc caa ccg tta	531			
Ser Leu Glu Asn His Leu Phe Arg Arg Gly Leu Tyr Phe Gln Pro Leu				
160 165 170				
tct tgg aaa ctt cgg ttg aaa gtt gct ctt ggt gct gca aag gga ctt	579			
Ser Trp Lys Leu Arg Leu Lys Val Ala Leu Gly Ala Lys Gly Leu				
175 180 185				
gct ttt ctt cac agt tcc gag aca aga gtg ata tac cga gat ttc aag	627			
Ala Phe Leu His Ser Ser Glu Thr Arg Val Ile Tyr Arg Asp Phe Lys				
190 195 200 205				
act tct aat atc ctt ctt gac tcg gag tac aac gca aag ctt tct gat	675			
Thr Ser Asn Ile Leu Leu Asp Ser Glu Tyr Asn Ala Lys Leu Ser Asp				
210 215 220				
ttt ggg ttg gct aag gat ggg cca ata ggt gat aaa agt cat gtc tct	723			
Phe Gly Leu Ala Lys Asp Gly Pro Ile Gly Asp Lys Ser His Val Ser				
225 230 235				
aca cga gtc atg ggt aca cac gga tat gca gct cct gaa tac ctt gca	771			
Thr Arg Val Met Gly Thr His Gly Tyr Ala Ala Pro Glu Tyr Leu Ala				
240 245 250				
acc ggt cat cta aca aca aag agt gat gtc tat agc ttc ggg gtt gtc	819			
Thr Gly His Leu Thr Thr Lys Ser Asp Val Tyr Ser Phe Gly Val Val				
255 260 265				
ctt ctg gag ctg ttg tct ggt cgt cga gca gtg gac aag aac cgc cca	867			
Leu Leu Glu Leu Leu Ser Gly Arg Arg Ala Val Asp Lys Asn Arg Pro				
270 275 280 285				
tct gga gag agg aac ctt gtg gag tgg gct aaa cca tac ctc gta aac	915			
Ser Gly Glu Arg Asn Leu Val Glu Trp Ala Lys Pro Tyr Leu Val Asn				
290 295 300				
aaa aga aag ata ttc cga gtc att gat aat cgt ctt cag gac cag tac	963			
Lys Arg Lys Ile Phe Arg Val Ile Asp Asn Arg Leu Gln Asp Gln Tyr				
305 310 315				
tct atg gaa gaa gca tgt aaa gtg gct act ctg tct ctg aga tgt ctc	1011			
Ser Met Glu Glu Ala Cys Lys Val Ala Thr Leu Ser Leu Arg Cys Leu				
320 325 330				
acc aca gag att aag ctg aga cca aac atg agc gag gtt gtt tcg cac	1059			
Thr Thr Glu Ile Lys Leu Arg Pro Asn Met Ser Glu Val Val Ser His				
335 340 345				

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350 355 360 365

aaa aca gat aga aga atg cgt agg aga agt gac agt gtt gtc agc aaa 1155
Lys Thr Asp Arg Arg Met Arg Arg Arg Ser Asp Ser Val Val Ser Lys
370 375 380

aaa gtg aat gca ggt ttt gct cga cag act gct gtt ggc agt aca gtt 1203
Lys Val Asn Ala Gly Phe Ala Arg Gln Thr Ala Val Gly Ser Thr Val
385 390 395

gtt gct tat cct cgc cca tca gcc tcg cca ctg tat gtt tga 1245
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 35 40 45

Gln Ser Pro Asn Leu Lys Ser Phe Ser Phe Ala Glu Leu Lys Ser Ala
 50 55 60

Thr Arg Asn Phe Arg Pro Asp Ser Val Leu Gly Glu Gly Gly Phe Gly
 65 70 75 80

Cys Val Phe Lys Gly Trp Ile Asp Glu Lys Ser Leu Thr Ala Ser Arg
 85 90 95

Pro Gly Thr Gly Leu Val Ile Ala Val Lys Lys Leu Asn Gln Asp Gly
 100 105 110

Trp Gln Gly His Gln Glu Trp Leu Ala Glu Val Asn Tyr Leu Gly Gln
 115 120 125

Phe Ser His Arg His Leu Val Lys Leu Ile Gly Tyr Cys Leu Glu Asp
 130 135 140

Glu His Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Gly Ser Leu Glu
 145 150 155 160

Asn His Leu Phe Arg Arg Gly Leu Tyr Phe Gln Pro Leu Ser Trp Lys

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His	Ser	Ser	Glu	Thr	Arg	Val	Ile	Tyr	Arg	Asp	Phe	Lys	Thr	Ser	Asn
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Ile	Leu	Leu	Asp	Ser	Glu	Tyr	Asn	Ala	Lys	Leu	Ser	Asp	Phe	Gly	Leu
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Ala	Lys	Asp	Gly	Pro	Ile	Gly	Asp	Lys	Ser	His	Val	Ser	Thr	Arg	Val
225					230					235					240
Met	Gly	Thr	His	Gly	Tyr	Ala	Ala	Pro	Glu	Tyr	Leu	Ala	Thr	Gly	His
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Leu	Thr	Thr	Lys	Ser	Asp	Val	Tyr	Ser	Phe	Gly	Val	Val	Leu	Leu	Glu
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Leu	Leu	Ser	Gly	Arg	Arg	Ala	Val	Asp	Lys	Asn	Arg	Pro	Ser	Gly	Glu
		275					280					285			
Arg	Asn	Leu	Val	Glu	Trp	Ala	Lys	Pro	Tyr	Leu	Val	Asn	Lys	Arg	Lys
	290					295					300				
Ile	Phe	Arg	Val	Ile	Asp	Asn	Arg	Leu	Gln	Asp	Gln	Tyr	Ser	Met	Glu
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Glu	Ala	Cys	Lys	Val	Ala	Thr	Leu	Ser	Leu	Arg	Cys	Leu	Thr	Thr	Glu
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Ile	Lys	Leu	Arg	Pro	Asn	Met	Ser	Glu	Val	Val	Ser	His	Leu	Glu	His
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Ile	Gln	Ser	Leu	Asn	Ala	Ala	Ile	Gly	Gly	Asn	Met	Asp	Lys	Thr	Asp
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Arg	Arg	Met	Arg	Arg	Arg	Ser	Asp	Ser	Val	Val	Ser	Lys	Lys	Val	Asn
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Ala	Gly	Phe	Ala	Arg	Gln	Thr	Ala	Val	Gly	Ser	Thr	Val	Val	Ala	Tyr
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 Met Leu Glu Lys Lys Leu Ala Ala Ala Glu Val Ser Glu Glu
 1 5 10

gag caa aat aac ttg cta aag gat ttg gag atg aag gaa act gaa tat 158
 Glu Gln Asn Asn Leu Leu Lys Asp Leu Glu Met Lys Glu Thr Glu Tyr
 15 20 25 30

atg cgc cgt cag agg cat aaa atg gga gct gat gac ttt gag cca ttg 206

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Thr Met Ile Gly Lys Gly Ala Phe Gly Glu
      50                      55

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ctgtgatgca tccttcttga aaggtcttct taggccattt tttttaccac agctaatttt 376
tcaaaaaagt atggcatgct aatttttctc tttctctttg cag gtt agg atc tgt 431
                        Val Arg Ile Cys
                        60

agg gag aag gga aca ggc aat gtc tat gca atg aag aag ctt aag aaa 479
Arg Glu Lys Gly Thr Gly Asn Val Tyr Ala Met Lys Lys Leu Lys Lys
      65                      70                      75

tct gag atg ctt cgc aga ggc cag gta tttaaattcc ttcaagtggc 526
Ser Glu Met Leu Arg Arg Gly Gln Val
      80                      85

tttcgtttga catttgttta gttggttgat gtgaatgtgg aatctgattt tcag gtg 583
                        Val

gaa cat gta aaa gca gag aga aat tta ctt gca gaa gtt gat agc aat 631
Glu His Val Lys Ala Glu Arg Asn Leu Leu Ala Glu Val Asp Ser Asn
      90                      95                      100

tgc att gtc aaa ctg tat tgt tct ttc caa gat gaa gag tac ttg tat 679
Cys Ile Val Lys Leu Tyr Cys Ser Phe Gln Asp Glu Glu Tyr Leu Tyr
      105                      110                      115

ctc ata atg gag tat tta cct ggt ggg gat atg atg act tta ctt atg 727
Leu Ile Met Glu Tyr Leu Pro Gly Gly Asp Met Met Thr Leu Leu Met
      120                      125                      130

agg aaa gac acc ctc act gaa gac gag gcc agg ttt tat att ggg gaa 775
Arg Lys Asp Thr Leu Thr Glu Asp Glu Ala Arg Phe Tyr Ile Gly Glu
      135                      140                      145                      150

act gtc ctg gct att gag tcc att cat aag cac aac tac att cac ag 822
Thr Val Leu Ala Ile Glu Ser Ile His Lys His Asn Tyr Ile His Ar
      155                      160                      165

gtcagtgaag cagaatatat gatttagttc tagctcccat tgttattttg ttctaaacgt 882
ctttttttct ccaatgtgat acag a gat atc aag cct gat aat ctg cta ctt 934
                        g Asp Ile Lys Pro Asp Asn Leu Leu Leu
                        s                      170                      175

gac aaa gac ggc cac atg aaa ttg tca gat ttt gga tta tgt aaa cca 982
Asp Lys Asp Gly His Met Lys Leu Ser Asp Phe Gly Leu Cys Lys Pro
      180                      185                      190

tta gac tgt agt aat ctt caa gag aaa gac ttt aca gtt gca aga aac 1030

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Leu Asp Cys Ser Asn Leu Gln Glu Lys Asp Phe Thr Val Ala Arg Asn
      195                                200                                205

gtt agt ggg gct tta caa agt gat ggt cgc cct gtg gcg aca aga cgc      1078
Val Ser Gly Ala Leu Gln Ser Asp Gly Arg Pro Val Ala Thr Arg Arg
      210                                215                                220

acc caa caa gag caa tta cta aac tgg cag aga aat aga agg atg ctt      1126
Thr Gln Gln Glu Gln Leu Leu Asn Trp Gln Arg Asn Arg Arg Met Leu
      225                                230                                235

gtaagtttca cttattcctc atcttttctt ccagagatgt ggagtagtcc acagtatcca 1186

gtatatattcg ttattgaaag caaattctct ccattgatat agacatctat gttagatatg 1246

acttactagg ttaaggatcat tacttttcag gct tat tcc aca gtt ggc act cct      1299
                                Ala Tyr Ser Thr Val Gly Thr Pro
                                240                                245

gac tat att gcc cca gaa gtt ctg ttg aaa aaa gga tat gga atg gaa      1347
Asp Tyr Ile Ala Pro Glu Val Leu Leu Lys Lys Gly Tyr Gly Met Glu
      250                                255                                260

tgt gat tg gtaggtgaag ccaacctatt cctattttgtg gtcttttgatt tcttttggtgt 1405
Cys Asp Tr
      265

aaataaataa tatgggtgaa taatcttgag atttag g tgg tct ctt ggc gcc att 1460
                                p Trp Ser Leu Gly Ala Ile
                                270

atg tat gaa atg ctt gtg ggg ttt ccg ccc ttt tat tca gat gac cca      1508
Met Tyr Glu Met Leu Val Gly Phe Pro Pro Phe Tyr Ser Asp Asp Pro
      275                                280                                285

atg aca act tgt agg aag gtaattaatc cattcctttt tgaatctttc      1556
Met Thr Thr Cys Arg Lys
      290

attttaatat tgaaggcaga ctggcgattt caagtcttac atttaatttt agtctttttg 1616

tatctcttttg gtaattctaa tgtggaaact tacctcttct cgattcatta tcttccccct 1676

tatgcag ata gta aat tgg aga aat tac ttg aaa ttc cca gat gag gtt      1725
      Ile Val Asn Trp Arg Asn Tyr Leu Lys Phe Pro Asp Glu Val
      295                                300                                305

aga cta tca cca gaa gcc aag gat ctt att tgt agg ctt tta tgc aat      1773
Arg Leu Ser Pro Glu Ala Lys Asp Leu Ile Cys Arg Leu Leu Cys Asn
      310                                315                                320

gtt gaa caa agg ctt gga aca aaa gga gca gat gaa att aag      1815
Val Glu Gln Arg Leu Gly Thr Lys Gly Ala Asp Glu Ile Lys
      325                                330                                335

gtgttgatg cgttggtcaa ctttgagatt caaagttccc ttatgtaaga tcattgtgtg 1875

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caattcttaa aaacgatttg actggtttct ttcag ggt cac cct tgg ttt aga 1928
                                Gly His Pro Trp Phe Arg
                                340

ggc aca gaa tgg gga aaa ttg tat caa atg aaa gct gcc ttt att ccc 1976
Gly Thr Glu Trp Gly Lys Leu Tyr Gln Met Lys Ala Ala Phe Ile Pro
345                                350                                355                                360

caa gtt aat gat gag ttg gac acc caa aat ttt gag aaa ttt gaa gag 2024
Gln Val Asn Asp Glu Leu Asp Thr Gln Asn Phe Glu Lys Phe Glu Glu
                                365                                370                                375

gtaacacact gatactatca gctaatagatg tctatagtga aatattggtg caatatatgc 2084

caccaaatga tgtggcatga tgtatatact gaaatattgg tatcacagat gatttttatg 2144

ctcctgataa ggaaaataat gtatactctt ctttgattcc ttctggaaca g act gac 2201
                                Thr Asp

aag caa gtt cca aag tca gcc aag tca ggt cca tgg aga aag 2243
Lys Gln Val Pro Lys Ser Ala Lys Ser Gly Pro Trp Arg Lys
380                                385                                390

gtacagcata agcactgact ttttggcatt atgtaccatc aagctttttt tttttatcta 2303

atagaagagt gatcatactt caaaatttat ctataagtgg gttccttgag atatgttggt 2363

ctttgatgat actacagacg tagcttaaaa tattacatgc aacaaagagc tcagaatgat 2423

gaaattggct cagtttctgt cacaggcggt tctatctttg tactatattc acaaaaacgt 2483

gattcactct tttaggttca aattttctta tggtaattha gaatttggag ctgattggga 2543

tgctactaac agaattatgt tgtaaatctg ccagttctgc atgttgacgt gtgttagatg 2603

aatcacttat ctttttggac caacatgata taacttagaa cctgttctgt caatagaatt 2663

tatgtcatga accaaaagga ttcttgtgaa tttcataaca tgacgctggc tttctttttt 2723

tcttctccag atg ctc tca tcc aaa gac att aac ttt gtt ggt tat act 2772
                                Met Leu Ser Ser Lys Asp Ile Asn Phe Val Gly Tyr Thr
                                395                                400                                405

tac aag aac gta gaa atc gta aat gat gac caa ata cca ggg ata g 2818
Tyr Lys Asn Val Glu Ile Val Asn Asp Asp Gln Ile Pro Gly Ile A
                                410                                415                                420

gtaattcact taacccccct tccgttgctg aggaagaagc aacaatacta gattaccttg 2878

tgattatcat cgcattgttg ctgcatttgt aatttgtttt attgtgcag ct gag ttg 2935
                                la Glu Leu
                                G

aag aag aag agc aat aag cca aaa agg ccg tct att aaa tct ctc ttt g 2984
Lys Lys Lys Ser Asn Lys Pro Lys Arg Pro Ser Ile Lys Ser Leu Phe G
225                                430                                435                                440

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<210> 70
<211> 476
<212> PRT
<213> Arabidopsis thaliana
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180					185					190					
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Ser	Gly	Ala	Leu	Gln	Ser	Asp	Gly	Arg	Pro	Val	Ala	Thr	Arg	Arg	Thr
	210					215					220				
Gln	Gln	Glu	Gln	Leu	Leu	Asn	Trp	Gln	Arg	Asn	Arg	Arg	Met	Leu	Ala
225					230					235					240
Tyr	Ser	Thr	Val	Gly	Thr	Pro	Asp	Tyr	Ile	Ala	Pro	Glu	Val	Leu	Leu
				245					250					255	
Lys	Lys	Gly	Tyr	Gly	Met	Glu	Cys	Asp	Trp	Trp	Ser	Leu	Gly	Ala	Ile
			260					265					270		
Met	Tyr	Glu	Met	Leu	Val	Gly	Phe	Pro	Pro	Phe	Tyr	Ser	Asp	Asp	Pro
		275					280					285			
Met	Thr	Thr	Cys	Arg	Lys	Ile	Val	Asn	Trp	Arg	Asn	Tyr	Leu	Lys	Phe
	290					295					300				
Pro	Asp	Glu	Val	Arg	Leu	Ser	Pro	Glu	Ala	Lys	Asp	Leu	Ile	Cys	Arg
305					310					315					320
Leu	Leu	Cys	Asn	Val	Glu	Gln	Arg	Leu	Gly	Thr	Lys	Gly	Ala	Asp	Glu
				325					330					335	
Ile	Lys	Gly	His	Pro	Trp	Phe	Arg	Gly	Thr	Glu	Trp	Gly	Lys	Leu	Tyr
			340					345					350		
Gln	Met	Lys	Ala	Ala	Phe	Ile	Pro	Gln	Val	Asn	Asp	Glu	Leu	Asp	Thr
		355					360					365			
Gln	Asn	Phe	Glu	Lys	Phe	Glu	Glu	Thr	Asp	Lys	Gln	Val	Pro	Lys	Ser
	370					375					380				
Ala	Lys	Ser	Gly	Pro	Trp	Arg	Lys	Met	Leu	Ser	Ser	Lys	Asp	Ile	Asn
385					390					395					400
Phe	Val	Gly	Tyr	Thr	Tyr	Lys	Asn	Val	Glu	Ile	Val	Asn	Asp	Asp	Gln
				405					410					415	
Ile	Pro	Gly	Ile	Ala	Glu	Leu	Lys	Lys	Lys	Ser	Asn	Lys	Pro	Lys	Arg
			420					425					430		
Pro	Ser	Ile	Lys	Ser	Leu	Phe	Glu	Asp	Glu	Thr	Ser	Gly	Gly	Thr	Thr
		435					440					445			
Thr	His	Gln	Gly	Ser	Phe	Leu	Asn	Leu	Leu	Pro	Thr	Gln	Ile	Glu	Asp
	450					455					460				
Pro	Glu	Lys	Glu	Gly	Ser	Lys	Ser	Ser	Ser	Ser	Gly				
465					470					475					

<210> 71
 <211> 979
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (28)..(843)

<400> 71
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 Met Ile Cys Arg Ile Arg Leu Gly Ser
 1 5

atg aac ggt gac gaa tgc gcg aac gtt gcg acg tgc tgg gtt act tct 102
 Met Asn Gly Asp Glu Cys Ala Asn Val Ala Thr Cys Trp Val Thr Ser
 10 15 20 25

cta gct tgt gta gtt gac gcc gga cga tat acg aaa aag gta tcc cac 150
 Leu Ala Cys Val Val Asp Ala Gly Arg Tyr Thr Lys Lys Val Ser His
 30 35 40

gac cgg cga acg agg tgg ccc gcc tgg aaa gca cga cgg gat cgt cat 198
 Asp Arg Arg Thr Arg Trp Pro Ala Trp Lys Ala Arg Arg Asp Arg His
 45 50 55

agt gtc cga agt gat agc ggc cta gac agt cat gca ctt gaa ggt gga 246
 Ser Val Arg Ser Asp Ser Gly Leu Asp Ser His Ala Leu Glu Gly Gly
 60 65 70

aaa cga cgt gag tca tgc gta tca cta gct cac gaa cga gat tat gca 294
 Lys Arg Arg Glu Ser Cys Val Ser Leu Ala His Glu Arg Asp Tyr Ala
 75 80 85

cta acg gca cgg tgg gat cgt agc att gca atg acg gat gac acg aac 342
 Leu Thr Ala Arg Trp Asp Arg Ser Ile Ala Met Thr Asp Asp Thr Asn
 90 95 100 105

cca caa acc caa cgt aaa ttt gag aaa cat act cgg gat gta gaa gct 390
 Pro Gln Thr Gln Arg Lys Phe Glu Lys His Thr Arg Asp Val Glu Ala
 110 115 120

gtt cga ttt tct cca cga gat cgt cta att gta tct gcg ggt gca gat 438
 Val Arg Phe Ser Pro Arg Asp Arg Leu Ile Val Ser Ala Gly Ala Asp
 125 130 135

ggg gta att gca gta tgt ccg gtt gct ggt gaa tgt gat gat gac gat 486
 Gly Val Ile Ala Val Cys Pro Val Ala Gly Glu Cys Asp Asp Asp Asp
 140 145 150

gcc cgt gat ggt cat gaa gat tgt gtt agt agt att tgc ttt tca cca 534
 Ala Arg Asp Gly His Glu Asp Cys Val Ser Ser Ile Cys Phe Ser Pro
 155 160 165

tca cta gaa cac ccg atc ctc ttt tct ggt agt tgt atc tac ttt att 582
 Ser Leu Glu His Pro Ile Leu Phe Ser Gly Ser Cys Ile Tyr Phe Ile

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170                      175                      180                      185
aaa gtg tgg aat gtc aat gga aag aaa tgt agg acg ccg cta aaa aag 630
Lys Val Trp Asn Val Asn Gly Lys Lys Cys Arg Thr Pro Leu Lys Lys
                      190                      195                      200

cat agt aat ccc gta tct aca cgg aca cag tca gaa gag gga agg cta 678
His Ser Asn Pro Val Ser Thr Arg Thr Gln Ser Glu Glu Gly Arg Leu
                      205                      210                      215

tgt gca aaa ggt ggt aaa agc ggt gca cgg cta cta ccc gat cta agt 726
Cys Ala Lys Gly Gly Lys Ser Gly Ala Arg Leu Leu Pro Asp Leu Ser
                      220                      225                      230

act cag gaa caa cta ccc aaa att aat caa gaa aac cct att aat caa 774
Thr Gln Glu Gln Leu Pro Lys Ile Asn Gln Glu Asn Pro Ile Asn Gln
                      235                      240                      245

att gct ttt tca cct agt ccg ttc gtc gtc acg tgc caa acg gaa aga 822
Ile Ala Phe Ser Pro Ser Pro Phe Val Val Thr Cys Gln Thr Glu Arg
250                      255                      260                      265

tcc cta tct caa acg tgg tga ccgtgcaccg gcacggtgaa aaagtcgacc 873
Ser Leu Ser Gln Thr Trp
                      270

ggatcgaccg accgaaagcc tgctcgctgg acaaaaaaag agcttttttag gcctttcgct 933
ttttttgaag aaaaaaggct cgcgaaaaaa aaaaagctcg aaatca 979

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<210> 72

<211> 271

<212> PRT

<213> Arabidopsis thaliana

<400> 72

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Met Ile Cys Arg Ile Arg Leu Gly Ser Met Asn Gly Asp Glu Cys Ala
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Asn Val Ala Thr Cys Trp Val Thr Ser Leu Ala Cys Val Val Asp Ala
          20           25           30

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Gly Arg Tyr Thr Lys Lys Val Ser His Asp Arg Arg Thr Arg Trp Pro
          35           40           45

```

```

Ala Trp Lys Ala Arg Arg Asp Arg His Ser Val Arg Ser Asp Ser Gly
          50           55           60

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Leu Asp Ser His Ala Leu Glu Gly Gly Lys Arg Arg Glu Ser Cys Val
          65           70           75           80

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Ser Leu Ala His Glu Arg Asp Tyr Ala Leu Thr Ala Arg Trp Asp Arg
          85           90           95

```

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Ser Ile Ala Met Thr Asp Asp Thr Asn Pro Gln Thr Gln Arg Lys Phe
          100          105          110

```

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Glu Lys His Thr Arg Asp Val Glu Ala Val Arg Phe Ser Pro Arg Asp
 115                      120                      125

Arg Leu Ile Val Ser Ala Gly Ala Asp Gly Val Ile Ala Val Cys Pro
 130                      135                      140

Val Ala Gly Glu Cys Asp Asp Asp Ala Arg Asp Gly His Glu Asp
 145                      150                      155                      160

Cys Val Ser Ser Ile Cys Phe Ser Pro Ser Leu Glu His Pro Ile Leu
                      165                      170                      175

Phe Ser Gly Ser Cys Ile Tyr Phe Ile Lys Val Trp Asn Val Asn Gly
                      180                      185                      190

Lys Lys Cys Arg Thr Pro Leu Lys Lys His Ser Asn Pro Val Ser Thr
 195                      200                      205

Arg Thr Gln Ser Glu Glu Gly Arg Leu Cys Ala Lys Gly Gly Lys Ser
 210                      215                      220

Gly Ala Arg Leu Leu Pro Asp Leu Ser Thr Gln Glu Gln Leu Pro Lys
 225                      230                      235                      240

Ile Asn Gln Glu Asn Pro Ile Asn Gln Ile Ala Phe Ser Pro Ser Pro
                      245                      250                      255

Phe Val Val Thr Cys Gln Thr Glu Arg Ser Leu Ser Gln Thr Trp
 260                      265                      270

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<210> 73
<211> 1260
<212> DNA
<213> Arabidopsis thaliana

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<220>
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<222> (101)..(155)

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<220>
<221> CDS
<222> (254)..(660)

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<220>
<221> CDS
<222> (750)..(1193)

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<400> 73
gctcaattat gtttacaaca ttgttgtaat ttcaaaactt cataagaatt tctctgataa 60

taaagaaaaa gctggagtag aactatttta aagtgtcatc atg aag aga cta agc 115
                      Met Lys Arg Leu Ser
                      1                      5

```

155

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agc tca gat tca atg tgt ggt cta atc tcc act tct aca g gttcttatta 165
Ser Ser Asp Ser Met Cys Gly Leu Ile Ser Thr Ser Thr A
      10                      15

ccatctttgt tctttctact ttttgcta at gtcagacaaa acccatgtga tcctttcttc 225

actttccact gtttctttta ttgacaag at tca ttt ggt tac aca aca gat gaa 279
      sp Ser Phe Gly Tyr Thr Thr Asp Glu
                20                      25

cag agt cca aga ggg tac gga agt aat tac caa tct atg ctt gaa ggt 327
Gln Ser Pro Arg Gly Tyr Gly Ser Asn Tyr Gln Ser Met Leu Glu Gly
      30                      35                      40

tac gat gaa gat gct aca cta atc gag gaa tat tcc ggc aac cac cac 375
Tyr Asp Glu Asp Ala Thr Leu Ile Glu Glu Tyr Ser Gly Asn His His
      45                      50                      55

cac atg ggt cta tcg gag aag aag aga aga tta aaa gtt gac caa gtc 423
His Met Gly Leu Ser Glu Lys Lys Arg Arg Leu Lys Val Asp Gln Val
      60                      65                      70                      75

aaa gct ctt gag aag aat ttc gaa ctt gag aat aaa ctc gaa cct gag 471
Lys Ala Leu Glu Lys Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu
      80                      85                      90

agg aaa act aaa tta gca caa gag ctt gga ctt caa cct cgt caa gta 519
Arg Lys Thr Lys Leu Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val
      95                      100                      105

gct gtt tgg ttt cag aac cgt cgt gca cgg tgg aaa aca aaa cag ctt 567
Ala Val Trp Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu
      110                      115                      120

gaa aaa gat tac ggt gtt ctt aag ggt caa tac gat tct ctc cgc cac 615
Glu Lys Asp Tyr Gly Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His
      125                      130                      135

aat ttc gat tct ctc cgc cgt gac aat gat tcc ctt ctc caa gag 660
Asn Phe Asp Ser Leu Arg Arg Asp Asn Asp Ser Leu Leu Gln Glu
      140                      145                      150

gtacaatatt agagacttta aaccataaaa attgaaactt cagagacgaa aatgcaaaaa 720

ggtttgattt ttaaagtttt tggttgcag att agt aaa atc aaa gct aag gta 773
      Ile Ser Lys Ile Lys Ala Lys Val
                155                      160

aac ggt gaa gaa gat aac aac aac aac aaa gct att acg gag ggt gtt 821
Asn Gly Glu Glu Asp Asn Asn Asn Asn Lys Ala Ile Thr Glu Gly Val
      165                      170                      175

aag gaa gag gaa gtt cac aag acg gat tcg att cct tcg tct cct ctg 869
Lys Glu Glu Glu Val His Lys Thr Asp Ser Ile Pro Ser Ser Pro Leu
      180                      185                      190

cag ttt cta gaa cat tcc tct ggt ttt aac tac cgg cga agc ttc act 917

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Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser Phe Thr
195                200                205                210

gac ctc cgt gac ctt cta ccg aat tcc acc gtt gtc gag gct gga tct    965
Asp Leu Arg Asp Leu Leu Pro Asn Ser Thr Val Val Glu Ala Gly Ser
                215                220                225

tcc gat agt tgc gat tca agc gcc gtt ctt aac gac gaa aca agt tct    1013
Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr Ser Ser
                230                235                240

gat aac gga aga ttg acg ccg cct gtg acg gtt act ggc ggg agt ttc    1061
Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly Ser Phe
                245                250                255

tta cag ttt gtg aaa aca gag caa aca gag gat cac gag gat ttt cta    1109
Leu Gln Phe Val Lys Thr Glu Gln Thr Glu Asp His Glu Asp Phe Leu
                260                265                270

agc ggt gaa gaa gct tgt ggt ttc ttc tcc gat gaa cag ccg ccg tca    1157
Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro Pro Ser
275                280                285                290

ctt cat tgg tac tct gct tca gat cat tgg act tga gaattgttta    1203
Leu His Trp Tyr Ser Ala Ser Asp His Trp Thr
                295                300

tcaaattggt gctctgttta gtctcaatgg gaaaacagag aagagggcaa aggtgga    1260

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<210> 74

<211> 301

<212> PRT

<213> Arabidopsis thaliana

<400> 74

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Met Lys Arg Leu Ser Ser Ser Asp Ser Met Cys Gly Leu Ile Ser Thr
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Ser Thr Asp Ser Phe Gly Tyr Thr Thr Asp Glu Gln Ser Pro Arg Gly
              20              25              30

Tyr Gly Ser Asn Tyr Gln Ser Met Leu Glu Gly Tyr Asp Glu Asp Ala
              35              40              45

Thr Leu Ile Glu Glu Tyr Ser Gly Asn His His His Met Gly Leu Ser
  50              55              60

Glu Lys Lys Arg Arg Leu Lys Val Asp Gln Val Lys Ala Leu Glu Lys
  65              70              75              80

Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu Arg Lys Thr Lys Leu
              85              90              95

Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val Ala Val Trp Phe Gln
              100              105              110

```

Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Lys Asp Tyr Gly
 115 120 125
 Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His Asn Phe Asp Ser Leu
 130 135 140
 Arg Arg Asp Asn Asp Ser Leu Leu Gln Glu Ile Ser Lys Ile Lys Ala
 145 150 155 160
 Lys Val Asn Gly Glu Glu Asp Asn Asn Asn Asn Lys Ala Ile Thr Glu
 165 170 175
 Gly Val Lys Glu Glu Glu Val His Lys Thr Asp Ser Ile Pro Ser Ser
 180 185 190
 Pro Leu Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser
 195 200 205
 Phe Thr Asp Leu Arg Asp Leu Leu Pro Asn Ser Thr Val Val Glu Ala
 210 215 220
 Gly Ser Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr
 225 230 235 240
 Ser Ser Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly
 245 250 255
 Ser Phe Leu Gln Phe Val Lys Thr Glu Gln Thr Glu Asp His Glu Asp
 260 265 270
 Phe Leu Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro
 275 280 285
 Pro Ser Leu His Trp Tyr Ser Ala Ser Asp His Trp Thr
 290 295 300

<210> 75

<211> 1122

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (22)..(1122)

<400> 75

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 Met Asn Gln Arg Ala Asp Arg Asp Arg Ala
 1 5 10

agc tcg atc cgt tgg ttt gcc aac cga tta gtg agt ggt agc ctg tta 99
 Ser Ser Ile Arg Trp Phe Ala Asn Arg Leu Val Ser Gly Ser Leu Leu
 15 20 25

ttg tgt gct aac gcc tac agt cgt cgt act ccc gcg tcc ggg gcc gca 147

Leu	Cys	Ala	Asn	Ala	Tyr	Ser	Arg	Arg	Thr	Pro	Ala	Ser	Gly	Ala	Ala		
			30					35					40				
tta	cag	cag	atg	aac	cgt	gcc	agt	cag	tca	gtg	aat	tac	cga	cga	cgt	195	
Leu	Gln	Gln	Met	Asn	Arg	Ala	Ser	Gln	Ser	Val	Asn	Tyr	Arg	Arg	Arg		
		45					50					55					
gag	ctg	tca	tta	atc	agc	ggc	cgg	aaa	cag	ggg	gtc	cag	tct	ctg	ggg	243	
Glu	Leu	Ser	Leu	Ile	Ser	Gly	Arg	Lys	Gln	Gly	Val	Gln	Ser	Leu	Gly		
	60					65					70						
tat	aga	ctt	gca	cgc	ctc	gat	aac	cgc	gct	ctt	gca	caa	ttg	ttg	cac	291	
Tyr	Arg	Leu	Ala	Arg	Leu	Asp	Asn	Arg	Ala	Leu	Ala	Gln	Leu	Leu	His		
	75				80					85					90		
agg	gat	ggc	cag	ccc	gag	gaa	gtg	gta	cag	cgc	ggc	aat	gaa	atc	agc	339	
Arg	Asp	Gly	Gln	Pro	Glu	Glu	Val	Val	Gln	Arg	Gly	Asn	Glu	Ile	Ser		
				95					100					105			
tat	ttc	gaa	acg	gga	ctt	gaa	ccg	acc	acg	ctt	aga	cgt	gtg	cgc	gat	387	
Tyr	Phe	Glu	Thr	Gly	Leu	Glu	Pro	Thr	Thr	Leu	Arg	Arg	Val	Arg	Asp		
			110					115					120				
tgt	gtt	gtt	gcc	gct	ctg	cca	acc	gtt	atc	tat	acc	gga	ttc	aaa	cgt	435	
Cys	Val	Val	Ala	Ala	Leu	Pro	Thr	Val	Ile	Tyr	Thr	Gly	Phe	Lys	Arg		
		125					130					135					
gtt	tct	cct	tac	tac	gaa	ttt	atc	tcc	gtc	ggg	cgc	acg	agg	gtt	gct	483	
Val	Ser	Pro	Tyr	Tyr	Glu	Phe	Ile	Ser	Val	Gly	Arg	Thr	Arg	Val	Ala		
	140					145					150						
gat	cgt	ctt	agc	gaa	gtc	acg	caa	gtg	gtt	ccc	cga	gat	gat	aca	cgc	531	
Asp	Arg	Leu	Ser	Glu	Val	Thr	Gln	Val	Val	Pro	Arg	Asp	Asp	Thr	Arg		
	155				160					165					170		
tac	gtc	tac	atc	gtg	tgg	cgg	gaa	tcc	gaa	cga	tcg	aaa	tta	gag	gcg	579	
Tyr	Val	Tyr	Ile	Val	Trp	Arg	Glu	Ser	Glu	Arg	Ser	Lys	Leu	Glu	Ala		
				175					180					185			
cgg	ggg	gat	ctc	cgt	gat	cgc	gat	ggg	gaa	acg	ctg	gaa	aag	ttt	cgc	627	
Arg	Gly	Asp	Leu	Arg	Asp	Arg	Asp	Gly	Glu	Thr	Leu	Glu	Lys	Phe	Arg		
			190					195					200				
gtg	att	gct	ttt	aac	gtc	acg	ctg	gat	atc	agc	agc	agt	atg	gag	ccg	675	
Val	Ile	Ala	Phe	Asn	Val	Thr	Leu	Asp	Ile	Ser	Ser	Ser	Met	Glu	Pro		
		205					210					215					
ctg	gcg	aag	gga	gat	ttg	ccg	ccg	ttg	ctt	gct	gtt	cct	gta	ggg	gaa	723	
Leu	Ala	Lys	Gly	Asp	Leu	Pro	Pro	Leu	Leu	Ala	Val	Pro	Val	Gly	Glu		
	220					225					230						
caa	gct	aga	ttc	agc	ttg	acg	cca	acc	tgg	ttg	cca	cag	ggg	cgt	agc	771	
Gln	Ala	Arg	Phe	Ser	Leu	Thr	Pro	Thr	Trp	Leu	Pro	Gln	Gly	Arg	Ser		
	235				240					245					250		
gat	gtt	tcc	agt	agt	cga	cgt	ggg	cta	ccg	cgg	atg	gac	aaa	gtg	cct	819	
Asp	Val	Ser	Ser	Ser	Arg	Arg	Gly	Leu	Pro	Arg	Met	Asp	Lys	Val	Pro		

255	260	265	
atc gaa tcc cgt ctc tcg acc gac gga gta ttc agc ttc tcg gta aac			867
Ile Glu Ser Arg Leu Ser Thr Asp Gly Val Phe Ser Phe Ser Val Asn			
270	275	280	
ggt aac ggc gct acg cca tcg agg tgg gat cag atg ttg cgc acc gga			915
Val Asn Gly Ala Thr Pro Ser Arg Trp Asp Gln Met Leu Arg Thr Gly			
285	290	295	
cgc agg ccc gtc agt aga agc gta cgt gat gtc gcc gaa aac acc att			963
Arg Arg Pro Val Ser Arg Ser Val Arg Asp Val Ala Glu Asn Thr Ile			
300	305	310	
ggc ggt gaa ctg ccg ccg cgt agc tgc tcg cga ccc gat ccg ttg acc			1011
Gly Gly Glu Leu Pro Pro Arg Ser Cys Ser Arg Pro Asp Pro Leu Thr			
315	320	325	330
gct gac cgc cga cgc tgc gct agc ctg agc ctg ccc agc ctg cca gct			1059
Ala Asp Arg Arg Arg Cys Ala Ser Leu Ser Leu Pro Ser Leu Pro Ala			
335	340	345	
cga cag ccc tcc caa acg gag aaa cgc att gtc gag aat att aag tac			1107
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Gly Ala Ala Pro			
365			

<210> 76

<211> 366

<212> PRT

<213> Arabidopsis thaliana

<400> 76

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			20					25				30		

Ser	Arg	Arg	Thr	Pro	Ala	Ser	Gly	Ala	Ala	Leu	Gln	Gln	Met	Asn	Arg
			35				40					45			

Ala	Ser	Gln	Ser	Val	Asn	Tyr	Arg	Arg	Arg	Glu	Leu	Ser	Leu	Ile	Ser
	50					55					60				

Gly	Arg	Lys	Gln	Gly	Val	Gln	Ser	Leu	Gly	Tyr	Arg	Leu	Ala	Arg	Leu
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Asp	Asn	Arg	Ala	Leu	Ala	Gln	Leu	Leu	His	Arg	Asp	Gly	Gln	Pro	Glu
			85						90					95	

Glu	Val	Val	Gln	Arg	Gly	Asn	Glu	Ile	Ser	Tyr	Phe	Glu	Thr	Gly	Leu
			100					105					110		

Glu Pro Thr Thr Leu Arg Arg Val Arg Asp Cys Val Val Ala Ala Leu
 115 120 125
 Pro Thr Val Ile Tyr Thr Gly Phe Lys Arg Val Ser Pro Tyr Tyr Glu
 130 135 140
 Phe Ile Ser Val Gly Arg Thr Arg Val Ala Asp Arg Leu Ser Glu Val
 145 150 155 160
 Thr Gln Val Val Pro Arg Asp Asp Thr Arg Tyr Val Tyr Ile Val Trp
 165 170 175
 Arg Glu Ser Glu Arg Ser Lys Leu Glu Ala Arg Gly Asp Leu Arg Asp
 180 185 190
 Arg Asp Gly Glu Thr Leu Glu Lys Phe Arg Val Ile Ala Phe Asn Val
 195 200 205
 Thr Leu Asp Ile Ser Ser Ser Met Glu Pro Leu Ala Lys Gly Asp Leu
 210 215 220
 Pro Pro Leu Leu Ala Val Pro Val Gly Glu Gln Ala Arg Phe Ser Leu
 225 230 235 240
 Thr Pro Thr Trp Leu Pro Gln Gly Arg Ser Asp Val Ser Ser Ser Arg
 245 250 255
 Arg Gly Leu Pro Arg Met Asp Lys Val Pro Ile Glu Ser Arg Leu Ser
 260 265 270
 Thr Asp Gly Val Phe Ser Phe Ser Val Asn Val Asn Gly Ala Thr Pro
 275 280 285
 Ser Arg Trp Asp Gln Met Leu Arg Thr Gly Arg Arg Pro Val Ser Arg
 290 295 300
 Ser Val Arg Asp Val Ala Glu Asn Thr Ile Gly Gly Glu Leu Pro Pro
 305 310 315 320
 Arg Ser Cys Ser Arg Pro Asp Pro Leu Thr Ala Asp Arg Arg Arg Cys
 325 330 335
 Ala Ser Leu Ser Leu Pro Ser Leu Pro Ala Arg Gln Pro Ser Gln Thr
 340 345 350
 Glu Lys Arg Ile Val Glu Asn Ile Lys Tyr Gly Ala Ala Pro
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<211> 1650

<212> DNA

<213> Arabidopsis thaliana

<220>

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Met Ser Met Asp Phe Ser Pro Leu Leu Thr Val																		
1 5 10																		
ctt gag gga gat ttc aac aag gat aat act tct tct gca aca gaa att																		101
Leu Glu Gly Asp Phe Asn Lys Asp Asn Thr Ser Ser Ala Thr Glu Ile																		
15 20 25																		
gat act tta gag aac tta gat gac act agg cag ata agt aaa gga aaa																		149
Asp Thr Leu Glu Asn Leu Asp Asp Thr Arg Gln Ile Ser Lys Gly Lys																		
30 35 40																		
cct ccg agg cac ctc aca agc agt gct act agg ctg cag ctt gca gcc																		197
Pro Pro Arg His Leu Thr Ser Ser Ala Thr Arg Leu Gln Leu Ala Ala																		
45 50 55																		
aat gcg gtaatatct tgacctgct tttctttttt cttttttcttt gttacaatgg																		253
Asn Ala																		
60																		
gattcgaatg atgtaactgg tttctgtttg tgcgcag gat gtg gat gtt tgt aac																		308
Asp Val Asp Val Cys Asn																		
65																		
ttg gtt atg aag tca ctt gat gac aaa tca gag ttt cta cct gta tac																		356
Leu Val Met Lys Ser Leu Asp Asp Lys Ser Glu Phe Leu Pro Val Tyr																		
70 75 80																		
cga tca gga agt tgt gct gag caa ggg gca aaa cag ttc atg gaa gat																		404
Arg Ser Gly Ser Cys Ala Glu Gln Gly Ala Lys Gln Phe Met Glu Asp																		
85 90 95																		
gaa cac att tgc atc gat gat ctt gtt aat cat ctt ggt gca gct att																		452
Glu His Ile Cys Ile Asp Asp Leu Val Asn His Leu Gly Ala Ala Ile																		
100 105 110 115																		
caa tgc tct tct ctt gga gcc ttc tat ggg gtgagtttat cttccaatct																		502
Gln Cys Ser Ser Leu Gly Ala Phe Tyr Gly																		
120 125																		
taccctaaaga agcataaaaag caattcacta gcctgattct tctttctttct cctctttttgt																		562

actagtacga tataagaggt attacttcaa aaactcttct aacatttggt gattgtgtgt 622

cctttggcag gta ttt gat ggc cac ggt ggc aca gat gca gca cac ttt 671
Val Phe Asp Gly His Gly Gly Thr Asp Ala Ala His Phe
130 135

gtt aga aag aac att ctg aga ttc att gta gag gac tcc tcc ttc cca 719
Val Arg Lys Asn Ile Leu Arg Phe Ile Val Glu Asp Ser Ser Phe Pro
140 145 150

cta tgc gta aag aaa gca att aag agt gct ttc tta aaa gct gat tat 767
Leu Cys Val Lys Lys Ala Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr
155 160 165 170

gaa ttt gca gat gat tct tct ctt gac atc tct tct ggg acc act gcg 815
Glu Phe Ala Asp Asp Ser Ser Leu Asp Ile Ser Ser Gly Thr Thr Ala
175 180 185

ctt aca gct ttt att ttt gga cg gtaagagcat ttaaattcgt atttatgaac 868
Leu Thr Ala Phe Ile Phe Gly Ar
190

ttgggaagct atatatgtta tcacctgtat aatcatcaat acttatcagg ttgcctgtgt 928

gtataagata gagaataagg cttagtgtaa agacttatgt aacgggctgt ttaccatgt 988

ttctttgtag ttttgatgtg attttgaata gaattgctac tttctttctt tacag g 1044
g

agg ttg ata att gca aat gct ggt gat tgc cga gca gta ctg ggg aga 1092
Arg Leu Ile Ile Ala Asn Ala Gly Asp Cys Arg Ala Val Leu Gly Arg
195 200 205 210

aga ggt agg gca att gag ttg tcc aaa gat cac aaa cca aac tgc aca 1140
Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn Cys Thr
215 220 225

gcc gag aaa gta aga ata gaa aag tta ggt gga gtt gtg tat gac ggt 1188
Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr Asp Gly
230 235 240

tac ctc aac ggg caa cta tca gtt gca cgt gcc att gga gac tgg cac 1236
Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp Trp His
245 250 255

atg aaa ggt ccc aaa ggc tct gct tgt ccg cta agc cca gag cca gag 1284
Met Lys Gly Pro Lys Gly Ser Ala Cys Pro Leu Ser Pro Glu Pro Glu
260 265 270

ttg caa gag aca gac ctg agt gaa gac gac gag ttc ttg ata atg gga 1332
Leu Gln Glu Thr Asp Leu Ser Glu Asp Asp Glu Phe Leu Ile Met Gly
275 280 285 290

tgt gat ggt ctg tgg gat gtg atg agc agc cag tgc gct gtg aca ata 1380
Cys Asp Gly Leu Trp Asp Val Met Ser Ser Gln Cys Ala Val Thr Ile
295 300 305

gct agg aag gaa ctg atg att cat aat gat cca gag aga tgc tct aga 1428
 Ala Arg Lys Glu Leu Met Ile His Asn Asp Pro Glu Arg Cys Ser Arg
 310 315 320
 gag ctt gtg agg gag gcc ctt aaa cgg aat aca tgt gac aat ttg aca 1476
 Glu Leu Val Arg Glu Ala Leu Lys Arg Asn Thr Cys Asp Asn Leu Thr
 325 330 335
 gtg att gtt gtg tgc ttc tct ccg gat cct cca cag agg ata gag atc 1524
 Val Ile Val Val Cys Phe Ser Pro Asp Pro Pro Gln Arg Ile Glu Ile
 340 345 350
 cga atg cag tca cgg gtg agg cgg agc ata tct gcg gaa ggg tta aac 1572
 Arg Met Gln Ser Arg Val Arg Arg Ser Ile Ser Ala Glu Gly Leu Asn
 355 360 365 370
 cta ctc aaa ggc gtg ctc gat ggc tat ccg tga gcatgttatg ttgtacgtta 1625
 Leu Leu Lys Gly Val Leu Asp Gly Tyr Pro
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 ctttgtgaga ctattgccaa gtttag 1650

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 20 25 30
 Leu Asp Asp Thr Arg Gln Ile Ser Lys Gly Lys Pro Pro Arg His Leu
 35 40 45
 Thr Ser Ser Ala Thr Arg Leu Gln Leu Ala Ala Asn Ala Asp Val Asp
 50 55 60
 Val Cys Asn Leu Val Met Lys Ser Leu Asp Asp Lys Ser Glu Phe Leu
 65 70 75 80
 Pro Val Tyr Arg Ser Gly Ser Cys Ala Glu Gln Gly Ala Lys Gln Phe
 85 90 95
 Met Glu Asp Glu His Ile Cys Ile Asp Asp Leu Val Asn His Leu Gly
 100 105 110
 Ala Ala Ile Gln Cys Ser Ser Leu Gly Ala Phe Tyr Gly Val Phe Asp
 115 120 125
 Gly His Gly Gly Thr Asp Ala Ala His Phe Val Arg Lys Asn Ile Leu
 130 135 140

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Arg Phe Ile Val Glu Asp Ser Ser Phe Pro Leu Cys Val Lys Lys Ala
145                      150                      155                      160

Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr Glu Phe Ala Asp Asp Ser
                      165                      170                      175

Ser Leu Asp Ile Ser Ser Gly Thr Thr Ala Leu Thr Ala Phe Ile Phe
                      180                      185                      190

Gly Arg Arg Leu Ile Ile Ala Asn Ala Gly Asp Cys Arg Ala Val Leu
                      195                      200                      205

Gly Arg Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn
210                      215                      220

Cys Thr Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr
225                      230                      235                      240

Asp Gly Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp
                      245                      250                      255

Trp His Met Lys Gly Pro Lys Gly Ser Ala Cys Pro Leu Ser Pro Glu
                      260                      265                      270

Pro Glu Leu Gln Glu Thr Asp Leu Ser Glu Asp Asp Glu Phe Leu Ile
                      275                      280                      285

Met Gly Cys Asp Gly Leu Trp Asp Val Met Ser Ser Gln Cys Ala Val
290                      295                      300

Thr Ile Ala Arg Lys Glu Leu Met Ile His Asn Asp Pro Glu Arg Cys
305                      310                      315                      320

Ser Arg Glu Leu Val Arg Glu Ala Leu Lys Arg Asn Thr Cys Asp Asn
                      325                      330                      335

Leu Thr Val Ile Val Val Cys Phe Ser Pro Asp Pro Pro Gln Arg Ile
                      340                      345                      350

Glu Ile Arg Met Gln Ser Arg Val Arg Arg Ser Ile Ser Ala Glu Gly
                      355                      360                      365

Leu Asn Leu Leu Lys Gly Val Leu Asp Gly Tyr Pro
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<210> 79

<211> 589

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (18)..(575)

<400> 79

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                  1                      5                      10

gag gtg cca aag gta gca aca gag gaa tca tcg gca gag gtt aca gat      98
Glu Val Pro Lys Val Ala Thr Glu Glu Ser Ser Ala Glu Val Thr Asp
                  15                      20                      25

cgt gga ttg ttc gat ttc ttg gga aag aag aaa gac gaa aca aaa cca     146
Arg Gly Leu Phe Asp Phe Leu Gly Lys Lys Lys Asp Glu Thr Lys Pro
                  30                      35                      40

gag gag act ccg atc gct tca gag ttt gag cag aag gtt cat att tca     194
Glu Glu Thr Pro Ile Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser
                  45                      50                      55

gag ccg gag cca gag gtt aaa cac gaa agt ctt ctt gaa aag ctt cac     242
Glu Pro Glu Pro Glu Val Lys His Glu Ser Leu Leu Glu Lys Leu His
                  60                      65                      70                      75

cga agc gac agt tct tct agc tcc tca agt gag gaa gaa ggt tca gat     290
Arg Ser Asp Ser Ser Ser Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp
                  80                      85                      90

ggt gag aag agg aag aag aag aag gag aag aag aag cca act act gaa     338
Gly Glu Lys Arg Lys Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu
                  95                      100                      105

gtt gag gta aag gag gaa gag aag aaa ggg ttt atg gag aag ttg aaa     386
Val Glu Val Lys Glu Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys
                  110                      115                      120

gag aag ctt cct gga cac aag aaa cct gaa gac ggt tca gcc gtc gct     434
Glu Lys Leu Pro Gly His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala
                  125                      130                      135

gcg gca ccg gtg gtt gtt cct cct cct gtg gaa gaa gcg cat cca gtg     482
Ala Ala Pro Val Val Val Pro Pro Pro Val Glu Glu Ala His Pro Val
                  140                      145                      150                      155

gag aag aaa ggg att ctt gag aag att aag gag aag ctt cca gga tac     530
Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Glu Lys Leu Pro Gly Tyr
                  160                      165                      170

cac cct aag acc acc gta gag gag gag aag aaa gat aaa gaa taa       575
His Pro Lys Thr Thr Val Glu Glu Glu Lys Lys Asp Lys Glu
                  175                      180                      185

gaagattatc attaa                                                    590

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<210> 80

<211> 185

<212> PRT

<213> Arabidopsis thaliana

<400> 80


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           20           25           30
Phe Leu Gly Lys Lys Lys Asp Glu Thr Lys Pro Glu Glu Thr Pro Ile
           35           40           45
Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser Glu Pro Glu Pro Glu
           50           55           60
Val Lys His Glu Ser Leu Leu Glu Lys Leu His Arg Ser Asp Ser Ser
           65           70           75           80
Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp Gly Glu Lys Arg Lys
           85           90           95
Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu Val Glu Val Lys Glu
           100           105           110
Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys Glu Lys Leu Pro Gly
           115           120           125
His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala Ala Ala Pro Val Val
           130           135           140
Val Pro Pro Pro Val Glu Glu Ala His Pro Val Glu Lys Lys Gly Ile
           145           150           155           160
Leu Glu Lys Ile Lys Glu Lys Leu Pro Gly Tyr His Pro Lys Thr Thr
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Val Glu Glu Glu Lys Lys Asp Lys Glu
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<210> 81
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 <212> DNA
 <213> Arabidopsis thaliana

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 <221> CDS
 <222> (20)..(1366)

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Glu Val Ala Ala Arg Leu Ala Ala Glu Asp Leu His Asp Ile Asn Lys
           15           20           25
tcc ggt ggt gct gat gtc aca atg tat aag gtg acg gag aga aca act 148

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Ser	Gly	Gly	Ala	Asp	Val	Thr	Met	Tyr	Lys	Val	Thr	Glu	Arg	Thr	Thr		
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gaa	cat	cca	ccg	gag	caa	gat	agg	ccc	ggt	gtg	ata	ggt	tca	gtg	ttc	196	
Glu	His	Pro	Pro	Glu	Gln	Asp	Arg	Pro	Gly	Val	Ile	Gly	Ser	Val	Phe		
	45					50				55							
agg	gct	gtc	caa	gga	acg	tat	gag	cat	gcg	aga	gac	gct	gta	gtt	gga	244	
Arg	Ala	Val	Gln	Gly	Thr	Tyr	Glu	His	Ala	Arg	Asp	Ala	Val	Val	Gly		
60				65					70					75			
aaa	acc	cac	gaa	gcg	gct	gag	tct	acc	aaa	gaa	gga	gct	cag	ata	gct	292	
Lys	Thr	His	Glu	Ala	Ala	Glu	Ser	Thr	Lys	Glu	Gly	Ala	Gln	Ile	Ala		
			80						85					90			
tca	gag	aaa	gcg	gtt	gga	gca	aag	gac	gca	acc	gtc	gag	aaa	gct	aag	340	
Ser	Glu	Lys	Ala	Val	Gly	Ala	Lys	Asp	Ala	Thr	Val	Glu	Lys	Ala	Lys		
			95					100					105				
gaa	acc	gct	gat	tat	act	gcg	gag	aag	gtg	ggt	gag	tat	aaa	gac	tat	388	
Glu	Thr	Ala	Asp	Tyr	Thr	Ala	Glu	Lys	Val	Gly	Glu	Tyr	Lys	Asp	Tyr		
		110					115					120					
acg	gtt	gat	aaa	gct	aaa	gag	gct	aag	gac	aca	act	gca	gag	aag	gcg	436	
Thr	Val	Asp	Lys	Ala	Lys	Glu	Ala	Lys	Asp	Thr	Thr	Ala	Glu	Lys	Ala		
		125				130					135						
aag	gag	act	gct	aat	tat	act	gcg	gat	aag	gcg	gtg	gaa	gca	aag	gat	484	
Lys	Glu	Thr	Ala	Asn	Tyr	Thr	Ala	Asp	Lys	Ala	Val	Glu	Ala	Lys	Asp		
140					145					150					155		
aag	acg	gcg	gag	aag	att	ggt	gag	tac	aaa	gac	tat	gcg	gtg	gat	aag	532	
Lys	Thr	Ala	Glu	Lys	Ile	Gly	Glu	Tyr	Lys	Asp	Tyr	Ala	Val	Asp	Lys		
				160					165					170			
gca	gta	gaa	gct	aaa	gat	aag	aca	gcg	gag	aag	gcg	aag	gag	act	tcg	580	
Ala	Val	Glu	Ala	Lys	Asp	Lys	Thr	Ala	Glu	Lys	Ala	Lys	Glu	Thr	Ser		
			175					180					185				
aat	tat	acg	gcg	gat	aag	gct	aaa	gag	gct	aag	gac	aag	acg	gct	gag	628	
Asn	Tyr	Thr	Ala	Asp	Lys	Ala	Lys	Glu	Ala	Lys	Asp	Lys	Thr	Ala	Glu		
		190					195					200					
aag	gtt	ggt	gag	tat	aag	gat	tac	acg	gtg	gac	aag	gcc	gtg	gaa	gct	676	
Lys	Val	Gly	Glu	Tyr	Lys	Asp	Tyr	Thr	Val	Asp	Lys	Ala	Val	Glu	Ala		
		205				210					215						
agg	gat	tac	aca	gcg	gag	aag	gct	att	gaa	gca	aag	gat	aag	aca	gct	724	
Arg	Asp	Tyr	Thr	Ala	Glu	Lys	Ala	Ile	Glu	Ala	Lys	Asp	Lys	Thr	Ala		
220					225					230				235			
gag	aag	act	gga	gag	tat	aag	gac	tat	acg	gtg	gag	aag	gcg	acg	gag	772	
Glu	Lys	Thr	Gly	Glu	Tyr	Lys	Asp	Tyr	Thr	Val	Glu	Lys	Ala	Thr	Glu		
				240					245					250			
ggg	aaa	gat	gtt	acg	gtg	agt	aag	cta	gga	gag	ctg	aag	gat	agt	gcc	820	
Gly	Lys	Asp	Val	Thr	Val	Ser	Lys	Leu	Gly	Glu	Leu	Lys	Asp	Ser	Ala		

255	260	265	
gtt gag aca gcg aag aga gct atg ggt ttc ttg tcg ggg aag aca gag			868
Val Glu Thr Ala Lys Arg Ala Met Gly Phe Leu Ser Gly Lys Thr Glu			
270	275	280	
gag gcc aaa gga aaa gct gtg gag acc aaa gat act gcc aag gaa aac			916
Glu Ala Lys Gly Lys Ala Val Glu Thr Lys Asp Thr Ala Lys Glu Asn			
285	290	295	
atg gag aaa gct gga gaa gta aca aga caa aag atg gag gaa atg aga			964
Met Glu Lys Ala Gly Glu Val Thr Arg Gln Lys Met Glu Glu Met Arg			
300	305	310	315
ttg gaa ggt aaa gag ctc aaa gaa gaa gct gga gca aaa gcc caa gag			1012
Leu Glu Gly Lys Glu Leu Lys Glu Glu Ala Gly Ala Lys Ala Gln Glu			
320	325	330	
gca tct caa aag act agg gag agt act gag tcg gga gct caa aaa gcc			1060
Ala Ser Gln Lys Thr Arg Glu Ser Thr Glu Ser Gly Ala Gln Lys Ala			
335	340	345	
gaa gag acc aaa gat tct cct gcc gtg agg gga aat gaa gcg aaa ggg			1108
Glu Glu Thr Lys Asp Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly			
350	355	360	
act att ttt ggt gca tta ggg aat gta acg gaa gca ata aag agc aaa			1156
Thr Ile Phe Gly Ala Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys			
365	370	375	
ctg aca atg cca tca gac att gtg gag gaa aca cgc gcg gca cgt gag			1204
Leu Thr Met Pro Ser Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu			
380	385	390	395
cat gga ggg acg ggt agg act gtg gtt gaa gtc aag gtc gag gat tca			1252
His Gly Gly Thr Gly Arg Thr Val Val Glu Val Lys Val Glu Asp Ser			
400	405	410	
aag ccg ggt aag gtg gcg act tca ctg aag gcg tcg gat caa atg acc			1300
Lys Pro Gly Lys Val Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr			
415	420	425	
ggt caa aca ttc aac gac gtt gga cgg atg gat gat gat gct cgg aaa			1348
Gly Gln Thr Phe Asn Asp Val Gly Arg Met Asp Asp Asp Ala Arg Lys			
430	435	440	
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Asp Lys Gly Lys Leu			
445			

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<211> 448

<212> PRT

<213> Arabidopsis thaliana

<400> 82

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          20           25           30
Val Thr Met Tyr Lys Val Thr Glu Arg Thr Thr Glu His Pro Pro Glu
          35           40           45
Gln Asp Arg Pro Gly Val Ile Gly Ser Val Phe Arg Ala Val Gln Gly
          50           55           60
Thr Tyr Glu His Ala Arg Asp Ala Val Val Gly Lys Thr His Glu Ala
 65           70           75           80
Ala Glu Ser Thr Lys Glu Gly Ala Gln Ile Ala Ser Glu Lys Ala Val
          85           90           95
Gly Ala Lys Asp Ala Thr Val Glu Lys Ala Lys Glu Thr Ala Asp Tyr
          100          105          110
Thr Ala Glu Lys Val Gly Glu Tyr Lys Asp Tyr Thr Val Asp Lys Ala
          115          120          125
Lys Glu Ala Lys Asp Thr Thr Ala Glu Lys Ala Lys Glu Thr Ala Asn
          130          135          140
Tyr Thr Ala Asp Lys Ala Val Glu Ala Lys Asp Lys Thr Ala Glu Lys
          145          150          155          160
Ile Gly Glu Tyr Lys Asp Tyr Ala Val Asp Lys Ala Val Glu Ala Lys
          165          170          175
Asp Lys Thr Ala Glu Lys Ala Lys Glu Thr Ser Asn Tyr Thr Ala Asp
          180          185          190
Lys Ala Lys Glu Ala Lys Asp Lys Thr Ala Glu Lys Val Gly Glu Tyr
          195          200          205
Lys Asp Tyr Thr Val Asp Lys Ala Val Glu Ala Arg Asp Tyr Thr Ala
          210          215          220
Glu Lys Ala Ile Glu Ala Lys Asp Lys Thr Ala Glu Lys Thr Gly Glu
          225          230          235          240
Tyr Lys Asp Tyr Thr Val Glu Lys Ala Thr Glu Gly Lys Asp Val Thr
          245          250          255
Val Ser Lys Leu Gly Glu Leu Lys Asp Ser Ala Val Glu Thr Ala Lys
          260          265          270
Arg Ala Met Gly Phe Leu Ser Gly Lys Thr Glu Glu Ala Lys Gly Lys
          275          280          285
Ala Val Glu Thr Lys Asp Thr Ala Lys Glu Asn Met Glu Lys Ala Gly
          290          295          300

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Glu Val Thr Arg Gln Lys Met Glu Glu Met Arg Leu Glu Gly Lys Glu
 305 310 315 320
 Leu Lys Glu Glu Ala Gly Ala Lys Ala Gln Glu Ala Ser Gln Lys Thr
 325 330 335
 Arg Glu Ser Thr Glu Ser Gly Ala Gln Lys Ala Glu Glu Thr Lys Asp
 340 345 350
 Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly Thr Ile Phe Gly Ala
 355 360 365
 Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys Leu Thr Met Pro Ser
 370 375 380
 Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu His Gly Gly Thr Gly
 385 390 395 400
 Arg Thr Val Val Glu Val Lys Val Glu Asp Ser Lys Pro Gly Lys Val
 405 410 415
 Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr Gly Gln Thr Phe Asn
 420 425 430
 Asp Val Gly Arg Met Asp Asp Asp Ala Arg Lys Asp Lys Gly Lys Leu
 435 440 445

<210> 83
 <211> 561
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (18)..(548)

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 1 5 10
 atc gta gta gca tta ttc ttc gat tta act caa gcc tat cgt cac act 98
 Ile Val Val Ala Leu Phe Phe Asp Leu Thr Gln Ala Tyr Arg His Thr
 15 20 25
 ccc gct caa ccg cca aaa gca aac gca aac ggt gat gtc aaa ccg caa 146
 Pro Ala Gln Pro Pro Lys Ala Asn Ala Asn Gly Asp Val Lys Pro Gln
 30 35 40
 gaa acg ctc gtg gtt cac aac aag gcc cga gcc atg gtc gga gtc gga 194
 Glu Thr Leu Val Val His Asn Lys Ala Arg Ala Met Val Gly Val Gly
 45 50 55
 cca atg gtg tgg aac gaa act ctt gcg acc tat gca cag agc tac gca 242
 Pro Met Val Trp Asn Glu Thr Leu Ala Thr Tyr Ala Gln Ser Tyr Ala

60	65	70	75	
cat gaa cga gcc aga gac tgt gcc atg aag cat tcc ttg gga cca ttc				290
His Glu Arg Ala Arg Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe	80	85	90	
ggc gag aat cta gcc gcg ggt tgg gga acg atg agc ggt ccg gta gca				338
Gly Glu Asn Leu Ala Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala	95	100	105	
act gag tat tgg atg acg gag aag gaa aat tac gat tat gat agt aac				386
Thr Glu Tyr Trp Met Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn	110	115	120	
acg tgt ggt ggt gat ggt gtg tgt gga cac tac act cag atc gtg tgg				434
Thr Cys Gly Gly Asp Gly Val Cys Gly His Tyr Thr Thr Gln Ile Val Trp	125	130	135	
cgt gac tcg gtt cga ctt ggt tgt gcc tcc gtg aga tgt aag aat gat				482
Arg Asp Ser Val Arg Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp	140	145	150	155
gag tat att tgg gtg att tgt agc tat gat cct ccg ggg aat tac atc				530
Glu Tyr Ile Trp Val Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile	160	165	170	
ggt caa cgt cca tat tag tgattggatt tta				561
Gly Gln Arg Pro Tyr	175			

<210> 84

<211> 176

<212> PRT

<213> Arabidopsis thaliana

<400> 84

Met Asn Glu Met Ser Phe Phe Gly Tyr Ser Phe Ile Val Val Ala Leu	1	5	10	15
Phe Phe Asp Leu Thr Gln Ala Tyr Arg His Thr Pro Ala Gln Pro Pro	20	25	30	
Lys Ala Asn Ala Asn Gly Asp Val Lys Pro Gln Glu Thr Leu Val Val	35	40	45	
His Asn Lys Ala Arg Ala Met Val Gly Val Gly Pro Met Val Trp Asn	50	55	60	
Glu Thr Leu Ala Thr Tyr Ala Gln Ser Tyr Ala His Glu Arg Ala Arg	65	70	75	80
Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe Gly Glu Asn Leu Ala	85	90	95	
Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala Thr Glu Tyr Trp Met	100	105	110	

Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn Thr Cys Gly Gly Asp
 115 120 125

Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp Arg Asp Ser Val Arg
 130 135 140

Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp Glu Tyr Ile Trp Val
 145 150 155 160

Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile Gly Gln Arg Pro Tyr
 165 170 175

<210> 85
 <211> 988
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (12)..(977)

<400> 85
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 Met Ala Ala Ser Lys Arg Leu Val Val Ser Cys Leu Phe
 1 5 10

tta gtt ttg ttg ttt gct caa gcc aat tcg caa ggt ttg aaa gta ggt 98
 Leu Val Leu Leu Phe Ala Gln Ala Asn Ser Gln Gly Leu Lys Val Gly
 15 20 25

ttc tac agc aaa aca tgc cca caa ctc gag ggt ata gtt aaa aag gtc 146
 Phe Tyr Ser Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val
 30 35 40 45

gtg ttc gat gcg atg aac aaa gca cca aca ctt ggt gct cct ttg ctt 194
 Val Phe Asp Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu
 50 55 60

aga atg ttc ttc cac gac tgc ttc gtt cgg gga tgt gac gga tca gtt 242
 Arg Met Phe Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val
 65 70 75

ttg tta gat aaa cca aac aat caa ggt gag aag agt gca gtt cct aac 290
 Leu Leu Asp Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn
 80 85 90

cta agt ctt cga ggg ttt ggc atc ata gac gat tcc aag gcg gct cta 338
 Leu Ser Leu Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu
 95 100 105

gaa aaa gtg tgt ccg gga att gtt tct tgc tct gat atc ttg gca ctt 386
 Glu Lys Val Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu
 110 115 120 125

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gtc gct aga gac gca atg gtt gca ctt gaa gga cca tca tgg gaa gtt 434
Val Ala Arg Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val
130 135 140

gaa acg gga aga aga gac ggt agg gtt tct aac atc aac gaa gtc aac 482
Glu Thr Gly Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn
145 150 155

ttg cca tca cct ttt gat aac atc acc aag ctt atc agc gat ttt cgc 530
Leu Pro Phe Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg
160 165 170

tca aag ggc ctc aac gag aag gat cta gtc att ctc tcg ggt ggt cac 578
Ser Lys Gly Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His
175 180 185

aca att gga atg gga cat tgt cct tta ttg aca aac cgg ctt tac aac 626
Thr Ile Gly Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn
190 195 200 205

ttc acc gga aaa gga gac agc gac cca agt ttg gac tcg gag tac gcc 674
Phe Thr Gly Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala
210 215 220

gct aag ctc agg aag aaa tgc aag ccc acc gat acg acg acg gct cta 722
Ala Lys Leu Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu
225 230 235

gag atg gat ccg ggg agt ttc aaa aca ttt gac ttg agc tac ttc acg 770
Glu Met Asp Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr
240 245 250

cta gtg gct aag aga aga gga ctt ttc cag tcg gat gct gct cta ctc 818
Leu Val Ala Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu
255 260 265

gac aac tcc aag act agg gct tat gtc ttg caa cag ata aga act cat 866
Asp Asn Ser Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His
270 275 280 285

ggg tca atg ttc ttt aac gac ttt ggt gtc tct atg gtg aaa atg ggt 914
Gly Ser Met Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly
290 295 300

cgg act gga gtt ctt acg ggt aag gcc ggg gag atc cgt aag acg tgt 962
Arg Thr Gly Val Leu Thr Gly Lys Ala Gly Glu Ile Arg Lys Thr Cys
305 310 315

cgg tct gct aat taa gagatataga aa 989
Arg Ser Ala Asn
320

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<210> 86

<211> 321

<212> PRT

<213> Arabidopsis thaliana

<400> 86

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Met Ala Ala Ser Lys Arg Leu Val Val Ser Cys Leu Phe Leu Val Leu
 1           5           10           15

Leu Phe Ala Gln Ala Asn Ser Gln Gly Leu Lys Val Gly Phe Tyr Ser
          20           25           30

Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val Val Phe Asp
      35           40           45

Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu Arg Met Phe
 50           55           60

Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Leu Asp
 65           70           75           80

Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn Leu Ser Leu
          85           90           95

Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu Glu Lys Val
      100           105           110

Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu Val Ala Arg
      115           120           125

Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val Glu Thr Gly
      130           135           140

Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn Leu Pro Ser
      145           150           155           160

Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg Ser Lys Gly
          165           170           175

Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His Thr Ile Gly
      180           185           190

Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn Phe Thr Gly
      195           200           205

Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala Ala Lys Leu
      210           215           220

Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu Glu Met Asp
      225           230           235           240

Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr Leu Val Ala
          245           250           255

Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu Asp Asn Ser
      260           265           270

Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His Gly Ser Met
      275           280           285

Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly Arg Thr Gly

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/28

290 295 300

Val Leu Thr Gly Lys Ala Gly Glu Ile Arg Lys Thr Cys Arg Ser Ala
305 310 315 320

Asn

<210> 87
<211> 650
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (8)..(634)

<400> 87

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1 5 10	
tcg ttc tcc tcc caa gtt tct caa aga cct aac acc att tcc ttc ccc	97
Ser Phe Ser Ser Gln Val Ser Gln Arg Pro Asn Thr Ile Ser Phe Pro	
15 20 25 30	
cgc gcg aat tca gta ttc gca tta ccg gcg aaa tcc gca cgc cgc gct	145
Arg Ala Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala	
35 40 45	
tct cta tct atc acc gcc acg gta tct gct cca ccg gag gag gag gag	193
Ser Leu Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu	
50 55 60	
ata gtt gaa ctg aag aaa tac gtc aaa tcg agg ctt ccc gga gga ttt	241
Ile Val Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe	
65 70 75	
gct gct cag aag att att ggc act gga cga cgt aag tgc gca atc gct	289
Ala Ala Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala	
80 85 90	
aga gtt gtt ctt cag gaa ggt act ggg aag gtt atc atc aac tat cgt	337
Arg Val Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg	
95 100 105 110	
gat gcc aag gag tac ctt cag gga aat cca ttg tgg ctt cag tat gtt	385
Asp Ala Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val	
115 120 125	
aaa gta cca ttg gtg act tta gga tat gag aat agc tac gac ata ttt	433
Lys Val Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe	
130 135 140	
gtg aaa gcc cat gga ggc ggt ctc tca ggt caa gct caa gca att acc	481
Val Lys Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr	

145	150	155	
ttg gga gtc gca cgt gca ctc ctg aag gta agt gca gac cac aga tcg			529
Leu Gly Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser			
160	165	170	
cct ttg aag aag gaa ggt ttg ctc act aga gat gcg aga gtg gtt gaa			577
Pro Leu Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu			
175	180	185	190
aga aag aag gcc ggg ctc aag aag gcg cgt aaa gcc cca caa ttc tcc			625
Arg Lys Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser			
195	200	205	
aag cgt taa gagttttata tatcat			650
Lys Arg			

<210> 88

<211> 208

<212> PRT

<213> Arabidopsis thaliana

<400> 88

Met Ala Ser Ile Thr Asn Leu Ala Ser Ser Leu Ser Ser Leu Ser Phe	
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20 25 30	
Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala Ser Leu	
35 40 45	
Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu Ile Val	
50 55 60	
Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe Ala Ala	
65 70 75 80	
Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala Arg Val	
85 90 95	
Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg Asp Ala	
100 105 110	
Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val Lys Val	
115 120 125	
Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe Val Lys	
130 135 140	
Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr Leu Gly	
145 150 155 160	
Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser Pro Leu	
165 170 175	

Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu Arg Lys
 180 185 190

Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser Lys Arg
 195 200 205

<210> 89

<211> 1223

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (16)..(1215)

<400> 89

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 1 5 10

gag atg gct cgg act cag aag aat aaa gct aca gag tat cat ctt ggt 99
 Glu Met Ala Arg Thr Gln Lys Asn Lys Ala Thr Glu Tyr His Leu Gly
 15 20 25

cag ctc aag gca aag att gca aaa ctc agg aca caa ctg ttg gag cct 147
 Gln Leu Lys Ala Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro
 30 35 40

cca aaa ggt gct agt gga ggc ggg gaa ggt ttt gaa gtt acc aag tat 195
 Pro Lys Gly Ala Ser Gly Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr
 45 50 55 60

ggt cat gga cgt gtt gca ctt ata gga ttt cct agt gtc gga aag tcc 243
 Gly His Gly Arg Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser
 65 70 75

acg ctt ttg act atg tta act gga aca cat tct gaa gca gcc tca tat 291
 Thr Leu Leu Thr Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr
 80 85 90

gaa ttt aca aca ctt aca tgc atc cct ggt gta att cac tac aac gac 339
 Glu Phe Thr Thr Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp
 95 100 105

aca aag att cag ctt ctc gat ctt cct ggg att att gaa ggt gct tcg 387
 Thr Lys Ile Gln Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser
 110 115 120

gaa gga aag ggg cga gga agg cag gtt att gct gtt gca aag tct tcc 435
 Glu Gly Lys Gly Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser
 125 130 135 140

gac ctt gta ttg atg gtt ctt gat gcc tca aaa agc gaa ggc cac agg 483
 Asp Leu Val Leu Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg
 145 150 155

caa ata ttg act aag gaa ctt gag gca gtg ggc ttg cga cta aac aaa	531
Gln Ile Leu Thr Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys	
160 165 170	
act cct ccg cag ata tac ttt aaa aag aaa aag act ggt gga atc tct	579
Thr Pro Pro Gln Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser	
175 180 185	
ttc aac act aca gca ccc ttg act cac att gat gag aag ctc tgt tat	627
Phe Asn Thr Thr Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr	
190 195 200	
caa atc ctg cat gaa tac aag att cac aat gct gag gtg cta ttt cgt	675
Gln Ile Leu His Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg	
205 210 215 220	
gag aat gcc aca gtg gat gac ttt att gat gtc att gaa ggc aac cgc	723
Glu Asn Ala Thr Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg	
225 230 235	
aag tat att aag tgt gtt tat gtc tac atc aaa ata gat gtt gtt gga	771
Lys Tyr Ile Lys Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly	
240 245 250	
att gat gat gtg gat aga cta tcc cgg cag cca aat tcc att gtt att	819
Ile Asp Asp Val Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile	
255 260 265	
agc tgc aat ctt aag ctt aac tta gac aga cta ctt gct agg atg tgg	867
Ser Cys Asn Leu Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp	
270 275 280	
gac gaa atg ggc ctt gtg aga gtt tac tcg aag ccg caa ggc cag caa	915
Asp Glu Met Gly Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln	
285 290 295 300	
cca gat ttc gat gag cct ttt gtc ctc tca tct gat cga ggt ggc tgc	963
Pro Asp Phe Asp Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys	
305 310 315	
aca gtg gaa gac ttc tgt aac cac gtc cac agg act ctg gtg aag gat	1011
Thr Val Glu Asp Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp	
320 325 330	
atg aag tat gca ctc gtt tgg ggc aca agc aca agg cac aat cca cag	1059
Met Lys Tyr Ala Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln	
335 340 345	
aat tgt ggt ctt tct caa cat ctt gaa gac gaa gat gtt gtt cag atc	1107
Asn Cys Gly Leu Ser Gln His Leu Glu Asp Glu Val Val Gln Ile	
350 355 360	
gtc aag aaa aag gag aga gac gaa gga gga aga ggc cgg ttc aag tca	1155
Val Lys Lys Lys Glu Arg Asp Glu Gly Gly Arg Gly Arg Phe Lys Ser	
365 370 375 380	

cac tca aac gcc cct gct aga att gca gac aga gag aaa aaa gct cct 1203
 His Ser Asn Ala Pro Ala Arg Ile Ala Asp Arg Glu Lys Lys Ala Pro
 385 390 395

ctt aag caa taa gcttttag 1223
 Leu Lys Gln
 400

<210> 90
 <211> 399
 <212> PRT
 <213> Arabidopsis thaliana

<400> 90
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 20 25 30
 Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro Pro Lys Gly Ala
 35 40 45
 Ser Gly Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr Gly His Gly Arg
 50 55 60
 Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser Thr Leu Leu Thr
 65 70 75 80
 Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr Glu Phe Thr Thr
 85 90 95
 Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp Thr Lys Ile Gln
 100 105 110
 Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser Glu Gly Lys Gly
 115 120 125
 Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser Asp Leu Val Leu
 130 135 140
 Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg Gln Ile Leu Thr
 145 150 155 160
 Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys Thr Pro Pro Gln
 165 170 175
 Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser Phe Asn Thr Thr
 180 185 190
 Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr Gln Ile Leu His
 195 200 205
 Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg Glu Asn Ala Thr
 210 215 220

Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg Lys Tyr Ile Lys
 225 230 235 240

Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly Ile Asp Asp Val
 245 250 255

Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile Ser Cys Asn Leu
 260 265 270

Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp Asp Glu Met Gly
 275 280 285

Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln Pro Asp Phe Asp
 290 295 300

Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys Thr Val Glu Asp
 305 310 315 320

Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp Met Lys Tyr Ala
 325 330 335

Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln Asn Cys Gly Leu
 340 345 350

Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile Val Lys Lys Lys
 355 360 365

Glu Arg Asp Glu Gly Gly Arg Gly Arg Phe Lys Ser His Ser Asn Ala
 370 375 380

Pro Ala Arg Ile Ala Asp Arg Glu Lys Lys Ala Pro Leu Lys Gln
 385 390 395

<210> 91
 <211> 536
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (12)..(524)

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 1 5 10

gtc tac ggc agt ttc caa gaa cca gcc gtt gtt aat tta att ctc gaa 98
 Val Tyr Gly Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu
 15 20 25

tgt gct ccg gtc atg gtt tcc gct caa ctc cac ggc tat cac ttg tat 146
 Cys Ala Pro Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr
 30 35 40 45

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aga ctt aaa ggt cgt ttg cat cca tgt att tct cct tcc gac aat gga 194
Arg Leu Lys Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly
      50                      55                      60

tta atc aat ggc aag ata cta act gga tta aca gat tct cag tta gag 242
Leu Ile Asn Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu
      65                      70                      75

agt tta gat atg att gaa gga act gaa tat gtg agg aag act gtt gaa 290
Ser Leu Asp Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu
      80                      85                      90

gtt gtt ttg act gat act ttg gag aag aag caa gtt gaa aca att gta 338
Val Val Leu Thr Asp Thr Leu Glu Lys Lys Gln Val Glu Thr Ile Val
      95                      100                      105

tgg gca aac aag gat gat cct aat atg tat gga gaa tgg gat ttc gag 386
Trp Ala Asn Lys Asp Asp Pro Asn Met Tyr Gly Glu Trp Asp Phe Glu
     110                      115                      120                      125

gaa tgg aag agg ctt cat atg gag aaa ttt ata gag gcg gcg acg aaa 434
Glu Trp Lys Arg Leu His Met Glu Lys Phe Ile Glu Ala Ala Thr Lys
      130                      135                      140

ttc atg gag tgg aag aag aat ccg aat ggg aga agt agg gaa gag ttt 482
Phe Met Glu Trp Lys Lys Asn Pro Asn Gly Arg Ser Arg Glu Glu Phe
      145                      150                      155

gag aag ttt gta caa gat gat tct tct ccg gct tcg gct tga 524
Glu Lys Phe Val Gln Asp Asp Ser Ser Pro Ala Ser Ala
      160                      165                      170

agaagttggtt ta 536

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<210> 92
 <211> 170
 <212> PRT
 <213> Arabidopsis thaliana

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<400> 92
Met Thr Ser Ser Asp Gln Ser Pro Ser His Asp Val Phe Val Tyr Gly
  1                      5                      10                      15

Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu Cys Ala Pro
      20                      25                      30

Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr Arg Leu Lys
      35                      40                      45

Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly Leu Ile Asn
      50                      55                      60

Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu Ser Leu Asp
      65                      70                      75                      80

Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu Val Val Leu

```


				85						90					95
Thr	Asp	Thr	Leu	Glu	Lys	Lys	Gln	Val	Glu	Thr	Ile	Val	Trp	Ala	Asn
			100					105					110		
Lys	Asp	Asp	Pro	Asn	Met	Tyr	Gly	Glu	Trp	Asp	Phe	Glu	Glu	Trp	Lys
			115				120					125			
Arg	Leu	His	Met	Glu	Lys	Phe	Ile	Glu	Ala	Ala	Thr	Lys	Phe	Met	Glu
	130					135					140				
Trp	Lys	Lys	Asn	Pro	Asn	Gly	Arg	Ser	Arg	Glu	Glu	Phe	Glu	Lys	Phe
145					150					155					160
Val	Gln	Asp	Asp	Ser	Ser	Pro	Ala	Ser	Ala						
				165				170							

<210> 93
 <211> 293
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (16)..(71)

<220>
 <221> CDS
 <222> (197)..(278)

<400> 93
 agagaagtaa gagaa atg gca ggt tct aac tgt gga tgt ggc tcc tcc tgc 51
 Met Ala Gly Ser Asn Cys Gly Cys Gly Ser Ser Cys
 1 5 10

aaa tgt ggt gat tgc tgc ag gtaaacccta gattctctct tcattaactt 101
 Lys Cys Gly Asp Ser Cys Se
 15

atcatgcata tatatcctaa tatacatgtg gttacatatt ccttaagata aattttgaaa 161

tcttatactt ctgttggtttt ttggtatga caaag t tgc gag aag aac tac aac 215
 r Cys Glu Lys Asn Tyr Asn
 20 25

aag gag tgt gat aac tgt agc tgt gga tca aac tgc agc tgc ggg tca 263
 Lys Glu Cys Asp Asn Cys Ser Cys Gly Ser Asn Cys Ser Cys Gly Ser
 30 35 40

agc tgt aac tgt tga agaaattatc agcat 293
 Ser Cys Asn Cys
 45

<210> 94

<211> 45

<212> PRT

<213> Arabidopsis thaliana

<400> 94

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Met Ala Gly Ser Asn Cys Gly Cys Gly Ser Ser Cys Lys Cys Gly Asp
 1             5             10             15

Ser Cys Ser Cys Glu Lys Asn Tyr Asn Lys Glu Cys Asp Asn Cys Ser
          20             25             30

Cys Gly Ser Asn Cys Ser Cys Gly Ser Ser Cys Asn Cys
      35             40             45

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<210> 95

<211> 880

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (14)..(868)

<400> 95

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cacaccaaca cca atg tct gct tct tct tta ttt aat ctc cca ttg att      49
          Met Ser Ala Ser Ser Leu Phe Asn Leu Pro Leu Ile
              1             5             10

cgc ctc aga tct ctc gct ctt tcg tct tct ttt tct tct ttc cga ttt      97
Arg Leu Arg Ser Leu Ala Leu Ser Ser Ser Phe Ser Ser Phe Arg Phe
      15             20             25

gcc cat cgt cct ctg tca tcg att tca ccg aga aag tta ccg aat ttt      145
Ala His Arg Pro Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe
      30             35             40

cgt gct ttc tct ggt acc gct atg aca gat act aaa gat gct ggt atg      193
Arg Ala Phe Ser Gly Thr Ala Met Thr Asp Thr Lys Asp Ala Gly Met
      45             50             55             60

gat gct gtt cag aga cgt ctc atg ttt gag gat gaa tgc att ctt gtt      241
Asp Ala Val Gln Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val
          65             70             75

gat gaa act gat cgt gtt gtg ggg cat gac agc aag tat aat tgt cat      289
Asp Glu Thr Asp Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His
          80             85             90

ctg atg gaa aat att gaa gcc aag aat ttg ctg cac agg gct ttt agt      337
Leu Met Glu Asn Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser
      95             100             105

gta ttt tta ttc aac tcg aag tat gag ttg ctt ctc cag caa agg tca      385
Val Phe Leu Phe Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser
      110             115             120

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aac aca aag gtt acg ttc cct cta gtg tgg act aac act tgt tgc agc 433
Asn Thr Lys Val Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser
125 130 135 140

cat cct ctt tac cgt gaa tca gag ctt atc cag gac aat gca cta ggt 481
His Pro Leu Tyr Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly
145 150 155

gtg agg aat gct gca caa aga aag ctt ctc gat gag ctt ggt att gta 529
Val Arg Asn Ala Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val
160 165 170

gct gaa gat gta cca gtc gat gag ttc act ccc ttg gga cgt atg ctg 577
Ala Glu Asp Val Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu
175 180 185

tac aag gct cct tct gat ggc aaa tgg gga gag cat gaa ctt gat tac 625
Tyr Lys Ala Pro Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr
190 195 200

ttg ctc ttc atc gtg cga gac gtg aag gtt caa cca aac cca gat gaa 673
Leu Leu Phe Ile Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu
205 210 215

gta gct gag atc aag tat gtg agc cgg gaa gag ctg aag gag ctg gtg 721
Val Ala Glu Ile Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val
225 230 235

aag aaa gca gat gca ggt gag gaa ggt ttg aaa ctg tca cca tgg ttc 769
Lys Lys Ala Asp Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe
240 245 250

aga ttg gtg gtg gac aat ttc ttg atg aag tgg tgg gat cat gta gag 817
Arg Leu Val Val Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu
255 260 265

aaa gga act ttg gtt gaa gct ata gac atg aaa acc atc cac aaa ctc 865
Lys Gly Thr Leu Val Glu Ala Ile Asp Met Lys Thr Ile His Lys Leu
270 275 280

tga acatcttttt tt 880

285

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<210> 96

<211> 284

<212> PRT

<213> Arabidopsis thaliana

<400> 96

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Met Ser Ala Ser Ser Leu Phe Asn Leu Pro Leu Ile Arg Leu Arg Ser
  1 5 10 15

Leu Ala Leu Ser Ser Ser Phe Ser Ser Phe Arg Phe Ala His Arg Pro
20 25 30

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Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe Arg Ala Phe Ser
 35 40 45
 Gly Thr Ala Met Thr Asp Thr Lys Asp Ala Gly Met Asp Ala Val Gln
 50 55 60
 Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val Asp Glu Thr Asp
 65 70 75 80
 Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Asn
 85 90 95
 Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe
 100 105 110
 Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser Asn Thr Lys Val
 115 120 125
 Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Tyr
 130 135 140
 Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly Val Arg Asn Ala
 145 150 155 160
 Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val Ala Glu Asp Val
 165 170 175
 Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu Tyr Lys Ala Pro
 180 185 190
 Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile
 195 200 205
 Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu Val Ala Glu Ile
 210 215 220
 Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val Lys Lys Ala Asp
 225 230 235 240
 Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe Arg Leu Val Val
 245 250 255
 Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu Lys Gly Thr Leu
 260 265 270
 Val Glu Ala Ile Asp Met Lys Thr Ile His Lys Leu
 275 280

<210> 97

<211> 831

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (18)..(821)

<400> 97

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tgcactactc aacctca atg gcc gcc tca aca atg gct ctc tcc tcc cct      50
          Met Ala Ala Ser Thr Met Ala Leu Ser Ser Pro
              1              5              10

gcc ttc gcc ggt aag gcc gtc aag ctt tcc ccc gcg gca tca gaa gtc      98
Ala Phe Ala Gly Lys Ala Val Lys Leu Ser Pro Ala Ala Ser Glu Val
          15              20              25

ctt gga agc ggc cgt gtg aca atg agg aag act gtt gcc aag cca aag     146
Leu Gly Ser Gly Arg Val Thr Met Arg Lys Thr Val Ala Lys Pro Lys
          30              35              40

ggc cca tca ggc agc cca tgg tac gga tct gac cgt gtc aag tac ttg     194
Gly Pro Ser Gly Ser Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu
          45              50              55

ggg cca ttc tct ggc gaa tca ccg agc tac ctt acc gga gag ttc ccc     242
Gly Pro Phe Ser Gly Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro
          60              65              70              75

gga gac tac gga tgg gac acc gcc gga ctt tca gct gac ccc gag aca     290
Gly Asp Tyr Gly Trp Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr
          80              85              90

ttc gca agg aac cgt gaa cta gaa gtt atc cac agc agg tgg gct atg     338
Phe Ala Arg Asn Arg Glu Leu Glu Val Ile His Ser Arg Trp Ala Met
          95              100              105

ctc gga gcc cta ggc tgc gtc ttc cct gag ctt ttg gct aga aac gga     386
Leu Gly Ala Leu Gly Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly
          110              115              120

gtc aag ttc gga gag gcg gtt tgg ttc aag gcc ggt tca cag atc ttc     434
Val Lys Phe Gly Glu Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe
          125              130              135

agc gat gga ggg ctc gat tac ttg gga aac cct agc ttg gtt cac gct     482
Ser Asp Gly Gly Leu Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala
          140              145              150              155

cag agc att ttg gcc att tgg gcc aca caa gtt att ttg atg gga gcc     530
Gln Ser Ile Leu Ala Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala
          160              165              170

gtt gaa ggc tac aga gtc gca gga aat ggg cca ttg gga gag gcc gag     578
Val Glu Gly Tyr Arg Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu
          175              180              185

gac ttg ctt tac ccc ggt ggc agc ttc gac cca ttg ggt ttg gct acc     626
Asp Leu Leu Tyr Pro Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr
          190              195              200

gac cca gag gca ttc gct gag ttg aag gtg aag gag ctc aag aac gga     674

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Asp Pro Glu Ala Phe Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly
205                210                215

aga ttg gct atg ttc tct atg ttt gga ttc ttc gtt caa gcc atc gtc 722
Arg Leu Ala Met Phe Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val
220                225                230                235

act ggt aag gga ccg ata gag aac ctt gct gac cat ttg gcc gat cca 770
Thr Gly Lys Gly Pro Ile Glu Asn Leu Ala Asp His Leu Ala Asp Pro
                240                245                250

gtt aac aac aac gca tgg gcc ttc gcc acc aac ttt gtt ccc gga aag 818
Val Asn Asn Asn Ala Trp Ala Phe Ala Thr Asn Phe Val Pro Gly Lys
                255                260                265

tga gccaaagtttt 831

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<210> 98
<211> 267
<212> PRT
<213> Arabidopsis thaliana

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<400> 98
Met Ala Ala Ser Thr Met Ala Leu Ser Ser Pro Ala Phe Ala Gly Lys
 1          5          10          15

Ala Val Lys Leu Ser Pro Ala Ala Ser Glu Val Leu Gly Ser Gly Arg
20          25          30

Val Thr Met Arg Lys Thr Val Ala Lys Pro Lys Gly Pro Ser Gly Ser
35          40          45

Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu Gly Pro Phe Ser Gly
50          55          60

Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro Gly Asp Tyr Gly Trp
65          70          75          80

Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr Phe Ala Arg Asn Arg
85          90          95

Glu Leu Glu Val Ile His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly
100         105         110

Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly Val Lys Phe Gly Glu
115         120         125

Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe Ser Asp Gly Gly Leu
130         135         140

Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala Gln Ser Ile Leu Ala
145         150         155         160

Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala Val Glu Gly Tyr Arg
165         170         175

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Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu Asp Leu Leu Tyr Pro
 180 185 190

Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr Asp Pro Glu Ala Phe
 195 200 205

Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly Arg Leu Ala Met Phe
 210 215 220

Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val Thr Gly Lys Gly Pro
 225 230 235 240

Ile Glu Asn Leu Ala Asp His Leu Ala Asp Pro Val Asn Asn Asn Ala
 245 250 255

Trp Ala Phe Ala Thr Asn Phe Val Pro Gly Lys
 260 265

<210> 99
 <211> 855
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (15)..(164)

<220>
 <221> CDS
 <222> (257)..(305)

<220>
 <221> CDS
 <222> (416)..(843)

<400> 99
 cacagtatta acaa atg gca gga atc aaa gtt ttc ggt cac cca gct tcc 50
 Met Ala Gly Ile Lys Val Phe Gly His Pro Ala Ser
 1 5 10

aca gcc act aga aga gtt ctc atc gct ctt cac gag aag aat gtc gac 98
 Thr Ala Thr Arg Arg Val Leu Ile Ala Leu His Glu Lys Asn Val Asp
 15 20 25

ttt gaa ttc gtt cat gtc gag ctc aaa gat ggt gaa cac aag aaa gag 146
 Phe Glu Phe Val His Val Glu Leu Lys Asp Gly Glu His Lys Lys Glu
 30 35 40

cct ttc atc ctt cgc aac gtgagtacat ataacatctg tcaagccaaa 194
 Pro Phe Ile Leu Arg Asn
 45 50

atattgtatt tcatttagat actgaatctt ggtcttaaca atcttgaata atgtttttgc 254

```

ag ccc ttt ggt aaa gtt cca gcc ttt gaa gat gga gac ttc aag att    301
  Pro Phe Gly Lys Val Pro Ala Phe Glu Asp Gly Asp Phe Lys Ile
                55                      60                      65

ttc g gtaaatacaa atatatatca ttatagtcac gtttacaaat ttttggtttt    355
Phe G

atgatcattg caataataga aagcagaaac actcaaaaat gttttttttt tgggtgggcag 415

aa tca aga gca att act caa tac ata gct cat gaa ttc tca gac aaa    462
lu Ser Arg Ala Ile Thr Gln Tyr Ile Ala His Glu Phe Ser Asp Lys
                70                      75                      80

gga aac aac ctt ctc tca act ggc aag gac atg gcg atc ata gcc atg    510
Gly Asn Asn Leu Leu Ser Thr Gly Lys Asp Met Ala Ile Ile Ala Met
                85                      90                      95

ggc att gaa att gag tcg cat gag ttt gac cca gtt ggt tca aag ctt    558
Gly Ile Glu Ile Glu Ser His Glu Phe Asp Pro Val Gly Ser Lys Leu
                100                     105                     110

gtt tgg gag caa gtc tta aag cct ttg tat ggt atg acc aca gac aaa    606
Val Trp Glu Gln Val Leu Lys Pro Leu Tyr Gly Met Thr Thr Asp Lys
                115                     120                     125

act gtt gtt gaa gaa gaa gag gct aag cta gcc aaa gtc ctc gat gtt    654
Thr Val Val Glu Glu Glu Glu Ala Lys Leu Ala Lys Val Leu Asp Val
                130                     135                     140                     145

tac gaa cac agg ctt ggt gag tcc aag tat ttg gct tct gac cac ttc    702
Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp His Phe
                150                     155                     160

act ttg gtc gat ctt cac act atc cct gtg att caa tac tta ctt gga    750
Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu Leu Gly
                165                     170                     175

act cca act aag aaa ctc ttc gac gag cgt cca cat gtg agt gct tgg    798
Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser Ala Trp
                180                     185                     190

gtt gct gac atc act tca agg cct tct gct cag aag gtt ctt taa    843
Val Ala Asp Ile Thr Ser Arg Pro Ser Ala Gln Lys Val Leu
                195                     200                     205

gtgaatctca aa                                                    855

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<210> 100

<211> 208

<212> PRT

<213> Arabidopsis thaliana

<400> 100

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Met Ala Gly Ile Lys Val Phe Gly His Pro Ala Ser Thr Ala Thr Arg
  1              5              10              15

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Arg Val Leu Ile Ala Leu His Glu Lys Asn Val Asp Phe Glu Phe Val
      20                      25                      30
His Val Glu Leu Lys Asp Gly Glu His Lys Lys Glu Pro Phe Ile Leu
      35                      40                      45
Arg Asn Pro Phe Gly Lys Val Pro Ala Phe Glu Asp Gly Asp Phe Lys
      50                      55                      60
Ile Phe Glu Ser Arg Ala Ile Thr Gln Tyr Ile Ala His Glu Phe Ser
      65                      70                      75                      80
Asp Lys Gly Asn Asn Leu Leu Ser Thr Gly Lys Asp Met Ala Ile Ile
      85                      90                      95
Ala Met Gly Ile Glu Ile Glu Ser His Glu Phe Asp Pro Val Gly Ser
      100                     105                     110
Lys Leu Val Trp Glu Gln Val Leu Lys Pro Leu Tyr Gly Met Thr Thr
      115                     120                     125
Asp Lys Thr Val Val Glu Glu Glu Glu Ala Lys Leu Ala Lys Val Leu
      130                     135                     140
Asp Val Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp
      145                     150                     155                     160
His Phe Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu
      165                     170                     175
Leu Gly Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser
      180                     185                     190
Ala Trp Val Ala Asp Ile Thr Ser Arg Pro Ser Ala Gln Lys Val Leu
      195                     200                     205

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<210> 101
<211> 512
<212> DNA
<213> Arabidopsis thaliana

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<220>
<221> CDS
<222> (12)..(67)

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<220>
<221> CDS
<222> (241)..(309)

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<220>
<221> CDS
<222> (417)..(492)

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<400> 101
tatctgaaaa a atg tca gag acc aac aag aat gcc ttc caa gcc ggt cag 50

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Met Ser Glu Thr Asn Lys Asn Ala Phe Gln Ala Gly Gln
 1 5 10

acc gct ggc aaa gct ga ggtactactc tttctctctt tgacagaact 97
 Thr Ala Gly Lys Ala Gl
 15

cttaaactgg aaaaattggt gaagctataa ctctttgaaa acagttgaaa cttgatcatt 157
 actagaaatt tcagttactt gtttaattta gtttgcgta attatgtaat tgatgatttt 217
 atggttacaa tgggtgtcat gta g gag aag agc aat gtt ctg ctg gac aag 268
 u Glu Lys Ser Asn Val Leu Leu Asp Lys
 20 25

gcc aag gat gct gca gct ggt gct gga gct gga gca caa ca ggtaaacaat 319
 Ala Lys Asp Ala Ala Ala Gly Ala Gly Ala Gln Gl
 30 35 40

ccatacacag acacataaca tataatatgt aacgaaataa acgtctttgt aagcttacat 379
 gtacgcagat ttctgatatg gttatgtata tggtata g gcg gga aag agt gta 432
 n Ala Gly Lys Ser Val
 45

tcg gat gcg gca gcg gga ggt gtt aac ttc gtg aag gac aag acc ggc 480
 Ser Asp Ala Ala Ala Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly
 50 55 60

ctg aac aag tag agattcgggt caaatttggg 512
 Leu Asn Lys
 65

<210> 102

<211> 66

<212> PRT

<213> Arabidopsis thaliana

<400> 102

Met Ser Glu Thr Asn Lys Asn Ala Phe Gln Ala Gly Gln Thr Ala Gly
 1 5 10 15

Lys Ala Glu Glu Lys Ser Asn Val Leu Leu Asp Lys Ala Lys Asp Ala
 20 25 30

Ala Ala Gly Ala Gly Ala Gly Ala Gln Gln Ala Gly Lys Ser Val Ser
 35 40 45

Asp Ala Ala Ala Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly Leu
 50 55 60

Asn Lys
 65

<210> 103
 <211> 1138
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (11)..(1123)

<400> 103
 aaaacaaaaa atg gcg act ttg gtt gat cct cct aat ggg ata agg aat 49
 Met Ala Thr Leu Val Asp Pro Pro Asn Gly Ile Arg Asn
 1 5 10

gaa ggg aag cat tac ttc tca atg tgg caa act ctg ttc gag atc gac 97
 Glu Gly Lys His Tyr Phe Ser Met Trp Gln Thr Leu Phe Glu Ile Asp
 15 20 25

act aag tac atg cct atc aag cct att ggt cgt gga gct tac ggt gtt 145
 Thr Lys Tyr Met Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val
 30 35 40 45

gtc tgc tcc tct gtt aac agt gac acc aac gag aaa gtt gct atc aag 193
 Val Cys Ser Ser Val Asn Ser Asp Thr Asn Glu Lys Val Ala Ile Lys
 50 55 60

aag att cac aat gtt tat gag aat agg atc gat gcg ttg agg act ctt 241
 Lys Ile His Asn Val Tyr Glu Asn Arg Ile Asp Ala Leu Arg Thr Leu
 65 70 75

cgg gag ctc aag ctt cta cgc cat ctt cga cat gag aat gtc att gct 289
 Arg Glu Leu Lys Leu Leu Arg His Leu Arg His Glu Asn Val Ile Ala
 80 85 90

ttg aaa gat gtc atg atg cca att cat aag atg agc ttc aag gat gtt 337
 Leu Lys Asp Val Met Met Pro Ile His Lys Met Ser Phe Lys Asp Val
 95 100 105

tat ctt gtt tat gag ctc atg gac act gat ctc cac cag att atc aag 385
 Tyr Leu Val Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys
 110 115 120 125

tct tct cag cgt ctt agt aac gat cat tgc caa tac ttc ttg ttc cag 433
 Ser Ser Gln Arg Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln
 130 135 140

ttg ctt cga ggg ctc aag tat att cat tca gcc aat atc ctg cac cga 481
 Leu Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Ile Leu His Arg
 145 150 155

gat ttg aaa cct ggt aac ctt ctt gtc aac gca aac tgc gat tta aag 529
 Asp Leu Lys Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys
 160 165 170

ata tgc gat ttt gga cta gcg cgt gcg agc aac acc aag ggt cag ttc 577
 Ile Cys Asp Phe Gly Leu Ala Arg Ala Ser Asn Thr Lys Gly Gln Phe
 175 180 185

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atg act gaa tat gtt gtg act cgt tgg tac cga gcc cca gag ctt ctc 625
Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu
190 195 200 205

ctc tgt tgt gac aac tat gga aca tcc att gat gtt tgg tct gtt ggt 673
Leu Cys Cys Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly
210 215 220

tgc att ttc gcc gag ctt ctt ggt agg aaa ccg ata ttc caa gga acg 721
Cys Ile Phe Ala Glu Leu Leu Gly Arg Lys Pro Ile Phe Gln Gly Thr
225 230 235

gaa tgt ctt aac cag ctt aag ctc att gtc aac att atc gga agc caa 769
Glu Cys Leu Asn Gln Leu Lys Leu Ile Val Asn Ile Ile Gly Ser Gln
240 245 250

aga gaa gaa gat ctt gag ttc ata gtt aac ccg aaa gct aaa aga tac 817
Arg Glu Glu Asp Leu Glu Phe Ile Val Asn Pro Lys Ala Lys Arg Tyr
255 260 265

att aga tca ctt ccg tac tca cct ggg atg tct tta tcc aga ctt tac 865
Ile Arg Ser Leu Pro Tyr Ser Pro Gly Met Ser Leu Ser Arg Leu Tyr
270 275 280 285

ccg tgc gct cat gta ttg gcc atc gac ctt ctg cag aaa atg ctt gtt 913
Pro Cys Ala His Val Leu Ala Ile Asp Leu Leu Gln Lys Met Leu Val
290 295 300

ttt gat ccg tca aag agg att agt gcc tct gaa gca ctc cag cat cca 961
Phe Asp Pro Ser Lys Arg Ile Ser Ala Ser Glu Ala Leu Gln His Pro
305 310 315

tac atg gcg cca cta tat gac ccg aat gca aac cct cct gct caa gtt 1009
Tyr Met Ala Pro Leu Tyr Asp Pro Asn Ala Asn Pro Pro Ala Gln Val
320 325 330

cct atc gat ctc gat gta gat gag gat ttg aga gag gag atg ata aga 1057
Pro Ile Asp Leu Asp Val Asp Glu Asp Leu Arg Glu Glu Met Ile Arg
335 340 345

gaa atg ata tgg aat gag atg ctt cac tac cat cca caa gct tca acc 1105
Glu Met Ile Trp Asn Glu Met Leu His Tyr His Pro Gln Ala Ser Thr
350 355 360 365

tta aac act gag ctc tga gctcaagtct tgttt 1138
Leu Asn Thr Glu Leu
370

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<210> 104

<211> 370

<212> PRT

<213> Arabidopsis thaliana

<400> 104

Met Ala Thr Leu Val Asp Pro Pro Asn Gly Ile Arg Asn Glu Gly Lys

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His Tyr Phe Ser Met Trp Gln Thr Leu Phe Glu Ile Asp Thr Lys Tyr	20	25	30
Met Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val Val Cys Ser	35	40	45
Ser Val Asn Ser Asp Thr Asn Glu Lys Val Ala Ile Lys Lys Ile His	50	55	60
Asn Val Tyr Glu Asn Arg Ile Asp Ala Leu Arg Thr Leu Arg Glu Leu	65	70	75
Lys Leu Leu Arg His Leu Arg His Glu Asn Val Ile Ala Leu Lys Asp	85	90	95
Val Met Met Pro Ile His Lys Met Ser Phe Lys Asp Val Tyr Leu Val	100	105	110
Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys Ser Ser Gln	115	120	125
Arg Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln Leu Leu Arg	130	135	140
Gly Leu Lys Tyr Ile His Ser Ala Asn Ile Leu His Arg Asp Leu Lys	145	150	155
Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys Ile Cys Asp	165	170	175
Phe Gly Leu Ala Arg Ala Ser Asn Thr Lys Gly Gln Phe Met Thr Glu	180	185	190
Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Leu Cys Cys	195	200	205
Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly Cys Ile Phe	210	215	220
Ala Glu Leu Leu Gly Arg Lys Pro Ile Phe Gln Gly Thr Glu Cys Leu	225	230	235
Asn Gln Leu Lys Leu Ile Val Asn Ile Ile Gly Ser Gln Arg Glu Glu	245	250	255
Asp Leu Glu Phe Ile Val Asn Pro Lys Ala Lys Arg Tyr Ile Arg Ser	260	265	270
Leu Pro Tyr Ser Pro Gly Met Ser Leu Ser Arg Leu Tyr Pro Cys Ala	275	280	285
His Val Leu Ala Ile Asp Leu Leu Gln Lys Met Leu Val Phe Asp Pro	290	295	300
Ser Lys Arg Ile Ser Ala Ser Glu Ala Leu Gln His Pro Tyr Met Ala			

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305                      310                      315                      320
Pro Leu Tyr Asp Pro Asn Ala Asn Pro Pro Ala Gln Val Pro Ile Asp
                      325                      330                      335
Leu Asp Val Asp Glu Asp Leu Arg Glu Glu Met Ile Arg Glu Met Ile
                      340                      345                      350
Trp Asn Glu Met Leu His Tyr His Pro Gln Ala Ser Thr Leu Asn Thr
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Glu Leu
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Ala Lys Thr Met Ala Ala Asn Lys Asp Lys Asp Lys Asp Lys Lys
                      15                      20                      25

ccc atc tct cgc tct gct cgt gct ggt att cag ttt cca gtt gga cga 148
Pro Ile Ser Arg Ser Ala Arg Ala Gly Ile Gln Phe Pro Val Gly Arg
                      30                      35                      40

att cac agg caa ctg aag acc cga gtc tcg gca cat ggc aga gtt ggt 196
Ile His Arg Gln Leu Lys Thr Arg Val Ser Ala His Gly Arg Val Gly
                      45                      50                      55

gcc act gca gcc gtc tac aca gct tca atc ctg gag tat ctg aca gca 244
Ala Thr Ala Ala Val Tyr Thr Ala Ser Ile Leu Glu Tyr Leu Thr Ala
                      60                      65                      70                      75

gag gtt ctt gag ttg gct ggg aat gcg agc aag gat ctc aaa gtg aag 292
Glu Val Leu Glu Leu Ala Gly Asn Ala Ser Lys Asp Leu Lys Val Lys
                      80                      85                      90

agg ata acg cca agg cat ctg cag ttg gcg att aga gga gat gag gag 340
Arg Ile Thr Pro Arg His Leu Gln Leu Ala Ile Arg Gly Asp Glu Glu
                      95                      100                      105

ctg gac aca ctc atc aag gga acg att gct gga ggt ggt gtg atc cct 388
Leu Asp Thr Leu Ile Lys Gly Thr Ile Ala Gly Gly Gly Val Ile Pro
                      110                      115                      120

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cac atc cac aag tct ctc atc aac aaa acc acc aag gag tga 430
 His Ile His Lys Ser Leu Ile Asn Lys Thr Thr Lys Glu
 125 130 135

tgtgtagctt tttat 445

<210> 106

<211> 136

<212> PRT

<213> Arabidopsis thaliana

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 20 25 30

Ala Arg Ala Gly Ile Gln Phe Pro Val Gly Arg Ile His Arg Gln Leu
 35 40 45

Lys Thr Arg Val Ser Ala His Gly Arg Val Gly Ala Thr Ala Ala Val
 50 55 60

Tyr Thr Ala Ser Ile Leu Glu Tyr Leu Thr Ala Glu Val Leu Glu Leu
 65 70 75 80

Ala Gly Asn Ala Ser Lys Asp Leu Lys Val Lys Arg Ile Thr Pro Arg
 85 90 95

His Leu Gln Leu Ala Ile Arg Gly Asp Glu Glu Leu Asp Thr Leu Ile
 100 105 110

Lys Gly Thr Ile Ala Gly Gly Gly Val Ile Pro His Ile His Lys Ser
 115 120 125

Leu Ile Asn Lys Thr Thr Lys Glu
 130 135

<210> 107

<211> 930

<212> DNA

<213> Arabidopsis thaliana

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<222> (14)..(916)

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 Met Tyr Leu Pro Lys Arg Gly Asn Leu Phe Glu Leu
 1 5 10

tat gat cca ttg cat cag aag atg tac aca ttg aat cta cct gag ctt	97
Tyr Asp Pro Leu His Gln Lys Met Tyr Thr Leu Asn Leu Pro Glu Leu	
15 20 25	
gcc aaa tct acg gtt tgt tac tca aga gat gga tgg tta cta atg cgt	145
Ala Lys Ser Thr Val Cys Tyr Ser Arg Asp Gly Trp Leu Leu Met Arg	
30 35 40	
aaa acc att tca aga gaa atg ttc ttc ttc aac ccg ttt act cgt gag	193
Lys Thr Ile Ser Arg Glu Met Phe Phe Phe Asn Pro Phe Thr Arg Glu	
45 50 55 60	
ctc ata aac gta cca aaa tgt act tta tca tat gat gcg atc gct ttc	241
Leu Ile Asn Val Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe	
65 70 75	
tct tgt gca cct aca tca ggt act tgc gtg ttg cta gca ttt aag cat	289
Ser Cys Ala Pro Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His	
80 85 90	
gtt tcg tat cgt atc acc act acg agc act tgc cat ccc aaa gca acc	337
Val Ser Tyr Arg Ile Thr Thr Thr Ser Thr Cys His Pro Lys Ala Thr	
95 100 105	
gag tgg gtt act gag gat cta caa ttc cat cgt cgc ttc cgc agt gaa	385
Glu Trp Val Thr Glu Asp Leu Gln Phe His Arg Arg Phe Arg Ser Glu	
110 115 120	
aca ctt aac cac agc aat gtt gtc tat gcc aaa cgt cgc ttc tat tgc	433
Thr Leu Asn His Ser Asn Val Val Tyr Ala Lys Arg Arg Phe Tyr Cys	
125 130 135 140	
ctt gac ggt caa gga agc tta tat tac ttt gat ccg tct tct cga aga	481
Leu Asp Gly Gln Gly Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg	
145 150 155	
tgg gat ttt agt tac acc tat tta ctg cca tgt cct tat atc tcg gat	529
Trp Asp Phe Ser Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp	
160 165 170	
aga ttt agt tac cag tat gag cgg aag aag aag aga att ttc ttg gct	577
Arg Phe Ser Tyr Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala	
175 180 185	
gtg cgg aaa gga gtg ttc ttt aag ata ttt aca tgt gat ggt gag aag	625
Val Arg Lys Gly Val Phe Phe Lys Ile Phe Thr Cys Asp Gly Glu Lys	
190 195 200	
ccg ata gtg cat aag tta gaa gat atc aat tgg gag gag atc aat agt	673
Pro Ile Val His Lys Leu Glu Asp Ile Asn Trp Glu Glu Ile Asn Ser	
205 210 215 220	
act acg att gat gga ttg aca atc ttt acg ggt ctt tat tcc tct gag	721
Thr Thr Ile Asp Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu	
225 230 235	
gtg aga ctt aat cta cca tgg atg agg aat agt gtt tac ttt cct aga	769


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Val Arg Leu Asn Leu Pro Trp Met Arg Asn Ser Val Tyr Phe Pro Arg
      240                      245                      250
ctt cgt ttt aat gtc aag cgt tgt gta tca tat tcg ctt gat gaa gag      817
Leu Arg Phe Asn Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu
      255                      260                      265

agg tat tat ccg cgg aag cag tgg caa gaa cag gag gat tta tgt cct      865
Arg Tyr Tyr Pro Arg Lys Gln Trp Gln Glu Gln Glu Asp Leu Cys Pro
      270                      275                      280

att gag aat ctt tgg att agg cca ccg aag aaa gct gta gat ttc atg      913
Ile Glu Asn Leu Trp Ile Arg Pro Pro Lys Lys Ala Val Asp Phe Met
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<210> 108
 <211> 300
 <212> PRT
 <213> Arabidopsis thaliana

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His Gln Lys Met Tyr Thr Leu Asn Leu Pro Glu Leu Ala Lys Ser Thr
      20                      25                      30

Val Cys Tyr Ser Arg Asp Gly Trp Leu Leu Met Arg Lys Thr Ile Ser
      35                      40                      45

Arg Glu Met Phe Phe Phe Asn Pro Phe Thr Arg Glu Leu Ile Asn Val
      50                      55                      60

Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe Ser Cys Ala Pro
      65                      70                      75                      80

Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His Val Ser Tyr Arg
      85                      90                      95

Ile Thr Thr Thr Ser Thr Cys His Pro Lys Ala Thr Glu Trp Val Thr
      100                     105                     110

Glu Asp Leu Gln Phe His Arg Arg Phe Arg Ser Glu Thr Leu Asn His
      115                     120                     125

Ser Asn Val Val Tyr Ala Lys Arg Arg Phe Tyr Cys Leu Asp Gly Gln
      130                     135                     140

Gly Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg Trp Asp Phe Ser
      145                     150                     155                     160

Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp Arg Phe Ser Tyr
      165                     170                     175

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Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala Val Arg Lys Gly
 180 185 190
 Val Phe Phe Lys Ile Phe Thr Cys Asp Gly Glu Lys Pro Ile Val His
 195 200 205
 Lys Leu Glu Asp Ile Asn Trp Glu Glu Ile Asn Ser Thr Thr Ile Asp
 210 215 220
 Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu Val Arg Leu Asn
 225 230 235 240
 Leu Pro Trp Met Arg Asn Ser Val Tyr Phe Pro Arg Leu Arg Phe Asn
 245 250 255
 Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu Arg Tyr Tyr Pro
 260 265 270
 Arg Lys Gln Trp Gln Glu Gln Glu Asp Leu Cys Pro Ile Glu Asn Leu
 275 280 285
 Trp Ile Arg Pro Pro Lys Lys Ala Val Asp Phe Met
 290 295 300

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gataccta	aaa	ccaaatccaa	ttca	atg	gcg	gaa	gaa	gca	aaa	tcc	aaa	gga	171			
				Met	Ala	Glu	Glu	Ala	Lys	Ser	Lys	Gly				
				1				5								
aac	gca	gct	ttc	tct	tcc	ggc	gat	tac	gcc	acc	gca	ata	acc	cat	ttc	219
Asn	Ala	Ala	Phe	Ser	Ser	Gly	Asp	Tyr	Ala	Thr	Ala	Ile	Thr	His	Phe	
10					15				20						25	
aca	gaa	gca	atc	aac	ctt	tca	cca	acc	aat	cac	atc	ctc	tac	tca	aac	267
Thr	Glu	Ala	Ile	Asn	Leu	Ser	Pro	Thr	Asn	His	Ile	Leu	Tyr	Ser	Asn	
				30					35						40	
aga	tcc	gct	tct	tac	gct	tct	ctc	cac	cgt	tac	gaa	gaa	gct	tta	tca	315
Arg	Ser	Ala	Ser	Tyr	Ala	Ser	Leu	His	Arg	Tyr	Glu	Glu	Ala	Leu	Ser	
				45				50						55		
gac	gcg	aag	aag	act	ata	gag	ctt	aaa	cct	gat	tgg	tct	aaa	gga	tat	363
Asp	Ala	Lys	Lys	Thr	Ile	Glu	Leu	Lys	Pro	Asp	Trp	Ser	Lys	Gly	Tyr	
		60					65					70				
agc	cga	tta	ggg	gct	gcg	ttt	att	gga	ttg	tcc	aag	ttt	gat	gaa	gcg	411
Ser	Arg	Leu	Gly	Ala	Ala	Phe	Ile	Gly	Leu	Ser	Lys	Phe	Asp	Glu	Ala	
	75					80					85					
gtt	gat	tcg	tat	aag	aaa	gga	tta	gag	att	gat	ccg	agt	aat	gag	atg	459
Val	Asp	Ser	Tyr	Lys	Lys	Gly	Leu	Glu	Ile	Asp	Pro	Ser	Asn	Glu	Met	
	90				95					100					105	
ctt	aaa	tcg	gga	tta	gct	gat	gct	tcg	aga	tct	agg	gtt	tcg	tca	aag	507
Leu	Lys	Ser	Gly	Leu	Ala	Asp	Ala	Ser	Arg	Ser	Arg	Val	Ser	Ser	Lys	
				110					115						120	
tcg	aat	cct	ttt	gtt	gat	gcg	ttt	caa	ggg	aag	gag	atg	tgg	gag	aag	555
Ser	Asn	Pro	Phe	Val	Asp	Ala	Phe	Gln	Gly	Lys	Glu	Met	Trp	Glu	Lys	
			125				130						135			
ttg	acg	gcg	gat	ccg	ggg	act	agg	gtt	tat	ttg	gag	cag	gat	gat	ttt	603
Leu	Thr	Ala	Asp	Pro	Gly	Thr	Arg	Val	Tyr	Leu	Glu	Gln	Asp	Asp	Phe	
		140					145					150				
gtt	aag	acg	atg	aag	gag	att	cag	agg	aac	cct	aat	aat	ctt	aat	ttg	651
Val	Lys	Thr	Met	Lys	Glu	Ile	Gln	Arg	Asn	Pro	Asn	Asn	Leu	Asn	Leu	
	155					160					165					
tat	atg	aag	gat	aag	aga	gtt	atg	aag	gct	tta	ggg	gtt	ttg	ttg	aat	699
Tyr	Met	Lys	Asp	Lys	Arg	Val	Met	Lys	Ala	Leu	Gly	Val	Leu	Leu	Asn	
	170				175					180					185	
gtg	aag	ttt	ggg	gga	tct	agt	ggg	gaa	gat	act	gag	atg	aag	gag	gct	747
Val	Lys	Phe	Gly	Gly	Ser	Ser	Gly	Glu	Asp	Thr	Glu	Met	Lys	Glu	Ala	
			190						195					200		
gat	gag	agg	aaa	gag	cct	gaa	ccg	gag	atg	gaa	cct	atg	gag	ttg	acg	795
Asp	Glu	Arg	Lys	Glu	Pro	Glu	Pro	Glu	Met	Glu	Pro	Met	Glu	Leu	Thr	
			205					210					215			
gag	gag	gag	agg	cag	aag	aag	gag	aga	aag	gag	aag	gct	ttg	aag	gag	843

Glu Glu Glu Arg Gln Lys Lys Glu Arg Lys Glu Lys Ala Leu Lys Glu
 220 225 230
 aaa ggg gaa gga aat gtt gct tat aag aag aag gat ttt ggg aga gct 891
 Lys Gly Glu Gly Asn Val Ala Tyr Lys Lys Lys Asp Phe Gly Arg Ala
 235 240 245
 gtt gaa cat tat act aag gcc atg gag ctc gat gat gag gat att tcg 939
 Val Glu His Tyr Thr Lys Ala Met Glu Leu Asp Asp Glu Asp Ile Ser
 250 255 260 265
 tat ttg acg aat cgt gct gct gtt tat ctt gag atg ggg aag 981
 Tyr Leu Thr Asn Arg Ala Ala Val Tyr Leu Glu Met Gly Lys
 270 275
 gtattaagtc ttataacttgg cttaaaagtt aaaccttttag gtactttaag attaaggagg 1041
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 ttgtgatgac cttgatgggt ttgataact ttcattctgct tcttggttga gatttaagag 1161
 ttttgaactt aagttttcac ttgtgctgaa agtagtttagc tttagatgag gtagaaattt 1221
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 gttcttgcac tagtcttgtt taattaacag ttgggttcac tggatcttac tgtatcttgt 1401
 gtgatgtttt acttcatttc tcaaatgaaa ttatcag tac gag gag tgc att gaa 1456
 Tyr Glu Glu Cys Ile Glu
 280 285
 gac tgt gac aag gct gtt gaa aga ggc aga gaa ctt cgt tct gac ttc 1504
 Asp Cys Asp Lys Ala Val Glu Arg Gly Arg Glu Leu Arg Ser Asp Phe
 290 295 300
 aag atg ata gca aga gct ctg act aga aaa gga tct gct cta gtg aaa 1552
 Lys Met Ile Ala Arg Ala Leu Thr Arg Lys Gly Ser Ala Leu Val Lys
 305 310 315
 atg gcg aga tgc tcg aaa gac ttt gag cct gcg att gag act ttc cag 1600
 Met Ala Arg Cys Ser Lys Asp Phe Glu Pro Ala Ile Glu Thr Phe Gln
 320 325 330
 aaa gct ctt aca gag cat cgt aat cca gat aca ttg aag aaa ctg aac 1648
 Lys Ala Leu Thr Glu His Arg Asn Pro Asp Thr Leu Lys Lys Leu Asn
 335 340 345
 gat gct gag aaa gtc aag aaa gag ctg gag caa cag gag tac ttt gat 1696
 Asp Ala Glu Lys Val Lys Lys Glu Leu Glu Gln Gln Glu Tyr Phe Asp
 350 355 360 365
 cct acg ata gcc gag gag gag cga gag aaa g gtatatatac tgatcctcag 1747
 Pro Thr Ile Ala Glu Glu Glu Arg Glu Lys G
 370 375

203

Val Gln Val Arg
555

gaagatgttt ccaaattttc actgcgttct tttgggcttt tgttaaactg atgaaactct 2618
gatttggttt gggatcatgtt tg 2640

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35 40 45
Leu His Arg Tyr Glu Glu Ala Leu Ser Asp Ala Lys Lys Thr Ile Glu
50 55 60
Leu Lys Pro Asp Trp Ser Lys Gly Tyr Ser Arg Leu Gly Ala Ala Phe
65 70 75 80
Ile Gly Leu Ser Lys Phe Asp Glu Ala Val Asp Ser Tyr Lys Lys Gly
85 90 95
Leu Glu Ile Asp Pro Ser Asn Glu Met Leu Lys Ser Gly Leu Ala Asp
100 105 110
Ala Ser Arg Ser Arg Val Ser Ser Lys Ser Asn Pro Phe Val Asp Ala
115 120 125
Phe Gln Gly Lys Glu Met Trp Glu Lys Leu Thr Ala Asp Pro Gly Thr
130 135 140
Arg Val Tyr Leu Glu Gln Asp Asp Phe Val Lys Thr Met Lys Glu Ile
145 150 155 160
Gln Arg Asn Pro Asn Asn Leu Asn Leu Tyr Met Lys Asp Lys Arg Val
165 170 175
Met Lys Ala Leu Gly Val Leu Leu Asn Val Lys Phe Gly Gly Ser Ser
180 185 190
Gly Glu Asp Thr Glu Met Lys Glu Ala Asp Glu Arg Lys Glu Pro Glu
195 200 205
Pro Glu Met Glu Pro Met Glu Leu Thr Glu Glu Glu Arg Gln Lys Lys
210 215 220
Glu Arg Lys Glu Lys Ala Leu Lys Glu Lys Gly Glu Gly Asn Val Ala

225		230		235		240
Tyr Lys Lys Lys Asp Phe Gly Arg Ala Val Glu His Tyr Thr Lys Ala	245	250	255			
Met Glu Leu Asp Asp Glu Asp Ile Ser Tyr Leu Thr Asn Arg Ala Ala	260	265	270			
Val Tyr Leu Glu Met Gly Lys Tyr Glu Glu Cys Ile Glu Asp Cys Asp	275	280	285			
Lys Ala Val Glu Arg Gly Arg Glu Leu Arg Ser Asp Phe Lys Met Ile	290	295	300			
Ala Arg Ala Leu Thr Arg Lys Gly Ser Ala Leu Val Lys Met Ala Arg	305	310	315			320
Cys Ser Lys Asp Phe Glu Pro Ala Ile Glu Thr Phe Gln Lys Ala Leu	325	330	335			
Thr Glu His Arg Asn Pro Asp Thr Leu Lys Lys Leu Asn Asp Ala Glu	340	345	350			
Lys Val Lys Lys Glu Leu Glu Gln Gln Glu Tyr Phe Asp Pro Thr Ile	355	360	365			
Ala Glu Glu Glu Arg Glu Lys Gly Asn Gly Phe Phe Lys Glu Gln Lys	370	375	380			
Tyr Pro Glu Ala Val Lys His Tyr Ser Glu Ala Ile Lys Arg Asn Pro	385	390	395			400
Asn Asp Val Arg Ala Tyr Ser Asn Arg Ala Ala Cys Tyr Thr Lys Leu	405	410	415			
Gly Ala Leu Pro Glu Gly Leu Lys Asp Ala Glu Lys Cys Ile Glu Leu	420	425	430			
Asp Pro Ser Phe Thr Lys Gly Tyr Ser Arg Lys Gly Ala Ile Gln Phe	435	440	445			
Phe Met Lys Glu Tyr Asp Lys Ala Met Glu Thr Tyr Gln Glu Gly Leu	450	455	460			
Lys His Asp Pro Lys Asn Gln Glu Phe Leu Asp Gly Val Arg Arg Cys	465	470	475			480
Val Glu Gln Ile Asn Lys Ala Ser Arg Gly Asp Leu Thr Pro Glu Glu	485	490	495			
Leu Lys Glu Arg Gln Ala Lys Ala Met Gln Asp Pro Glu Val Gln Asn	500	505	510			
Ile Leu Ser Asp Pro Val Met Arg Gln Val Leu Val Asp Phe Gln Glu	515	520	525			
Asn Pro Lys Ala Ala Gln Glu His Met Lys Asn Pro Met Val Met Asn						

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530                               535                               540
Lys Ile Gln Lys Leu Val Ser Ala Gly Ile Val Gln Val Arg
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atcaagaaa atg gga aga gca ccg tgt tgt gat aag gcc aac gtg aag aaa 171
      Met Gly Arg Ala Pro Cys Cys Asp Lys Ala Asn Val Lys Lys
           1             5             10
ggg cct tgg tct cct gag gaa gac gcc aaa ctc aaa gat tac atc gag 219
Gly Pro Trp Ser Pro Glu Glu Asp Ala Lys Leu Lys Asp Tyr Ile Glu
15             20             25             30
aat agt ggc aca gga ggc aac tgg att gct ttg cct cag aaa att g 265
Asn Ser Gly Thr Gly Gly Asn Trp Ile Ala Leu Pro Gln Lys Ile G
           35             40             45
gtatgtatta cttaaaactc actttttgatt taaaattggc actgagagtt tccaaatagt 325
actttgagac cgtgggtcgtg ttaaatttgt gtgttgatga tattttattta catggtatag 385
gt tta agg aga tgt ggg aag agt tgc agg cta agg tgg ctc aac tat 432
ly Leu Arg Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr
           50             55             60
ttg aga cca aac atc aaa cat ggt ggc ttc tcc gag gaa gaa gac aac 480
Leu Arg Pro Asn Ile Lys His Gly Gly Phe Ser Glu Glu Glu Asp Asn
           65             70             75
atc att tgt aac ctc tat gtt act att ggt agc ag gtactatata 525
Ile Ile Cys Asn Leu Tyr Val Thr Ile Gly Ser Ar
           80             85

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cttacatata tatcatcata tgcattgatg aatattatta attgacacac ttattcttga 585
cttagagact cactatgtat ctttgttttaa ttctag g tgg tct ata att gct gca 640
                                     g Trp Ser Ile Ile Ala Ala
                                     90                               95

caa ttg ccg gga aga acc gac aac gat atc aaa aac tat tgg aac acg 688
Gln Leu Pro Gly Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr
                                     100                               110

agg ctg aag aag aag ctt ctg aac aaa caa agg aaa gag ttc caa gaa 736
Arg Leu Lys Lys Lys Leu Leu Asn Lys Gln Arg Lys Glu Phe Gln Glu
                                     115                               120

gcg cga atg aag caa gag atg gtg atg atg aaa agg caa caa caa gga 784
Ala Arg Met Lys Gln Glu Met Val Met Met Lys Arg Gln Gln Gly
                                     130                               140

caa gga caa ggt caa agt aat ggt agt acg gat ctt tat ctt aac aac 832
Gln Gly Gln Gly Gln Ser Asn Gly Ser Thr Asp Leu Tyr Leu Asn Asn
                                     145                               155

atg ttt gga tca tca cca tgg cca tta cta cca caa ctt cct cct cca 880
Met Phe Gly Ser Ser Pro Trp Pro Leu Leu Pro Gln Leu Pro Pro Pro
160                                     165                               170

cat cat caa ata cct ctt gga atg atg gaa cca aca agc tgt aac tac 928
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Leu Lys Asn Met Val Lys Ile Glu Glu Glu Gln Glu Arg Thr Asn Pro
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225                                     230                               235

tct cag ctt ttg tta gat ccc aat tac tat ctg gga tca gga ggg gga 1120
Ser Gln Leu Leu Leu Asp Pro Asn Tyr Tyr Leu Gly Ser Gly Gly Gly
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Thr Lys Val Tyr Gly Asp Ala Ser Val Ala Gly Ala Ala Val Arg Ala
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85 90 95

Leu Pro Gly Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr Arg
100 105 110

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130 135 140

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 His Gln Ile Pro Leu Gly Met Met Glu Pro Thr Ser Cys Asn Tyr Tyr
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 Lys Asn Met Val Lys Ile Glu Glu Glu Gln Glu Arg Thr Asn Pro Asp
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 His His His Gln Asp Ser Val Thr Asn Pro Phe Asp Phe Ser Phe Ser
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 Glu Gly Asp Phe Ala Ile Met Ser Ser Ser Thr Asn Ser Pro Leu Pro
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cgt caa atg gaa gac gga aaa gct atc cag ctc gtc ctt gat cag agc      147
Arg Gln Met Glu Asp Gly Lys Ala Ile Gln Leu Val Leu Asp Gln Ser
             30             35             40

act g gtacaccaac gccacagtta tatttttaaa cggaaacatt ttgaaattaa      201
Thr G

tggtgTTTTt atgtaatata ctctcactgt acatgttcat atttgtcttt taaag ga      258
                        ly

tgt gga ttt gct tcc aaa aga aaa tat cta ttc gga cga gtg agc atg      306
Cys Gly Phe Ala Ser Lys Arg Lys Tyr Leu Phe Gly Arg Val Ser Met
  45             50             55

aag atc aaa ctc att ccc gga gac tct gcc ggt acg gtc acc gct ttc      354
Lys Ile Lys Leu Ile Pro Gly Asp Ser Ala Gly Thr Val Thr Ala Phe
  60             65             70             75

tac gtaagtctat cattttactc cactagtttt gaaattttac acattcacac      407
Tyr

aataaaaaaat aacattttct tgaaacacta acgggtcaaat cattgatatg tctatag      464

atg aac tcc gat acg gcc acg gtg aga gac gag cta gat ttt gag ttc      512
Met Asn Ser Asp Thr Ala Thr Val Arg Asp Glu Leu Asp Phe Glu Phe
             80             85             90

ttg gga aac aga agt ggt caa cct tac tca gtg caa aca aac ata ttt      560
Leu Gly Asn Arg Ser Gly Gln Pro Tyr Ser Val Gln Thr Asn Ile Phe
             95             100             105

gct cat ggc aaa gga gat aga gaa caa aga gtt aat ctt tgg ttc gac      608
Ala His Gly Lys Gly Asp Arg Glu Gln Arg Val Asn Leu Trp Phe Asp
  110             115             120

cca tct atg gat tac cac act tac act atc tta tgg tca cac aaa cac      656
Pro Ser Met Asp Tyr His Thr Tyr Thr Ile Leu Trp Ser His Lys His
  125             130             135             140

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att gtg taagcttttc tctaattgta ctttcaacta gaatcaacat ttactgtttc      712
Ile Val

aaaacaaaaa atcaccattt actgttttaaa aaaaccttag tttaacgtgg ggttggttttg 772

gttactcagt ttt tac gta gac gat gtg cca ata aga gaa tac aaa aac      821
      Phe Tyr Val Asp Asp Val Pro Ile Arg Glu Tyr Lys Asn
      145                      150                      155

aac gaa gcc aag aac ata gct tac cca aca tca caa cct atg gga gta      869
Asn Glu Ala Lys Asn Ile Ala Tyr Pro Thr Ser Gln Pro Met Gly Val
      160                      165                      170

tac tca aca tta tgg gaa gca gat gac tgg gca aca cgt ggt gga tta      917
Tyr Ser Thr Leu Trp Glu Ala Asp Asp Trp Ala Thr Arg Gly Gly Leu
      175                      180                      185

gag aaa att gat tgg agc aaa gct cca ttt tat gct tat tac aaa gat      965
Glu Lys Ile Asp Trp Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr Lys Asp
      190                      195                      200

ttc gac atc gaa ggt tgt cct gtt cct gga cca acc ttt tgt cca tcg      1013
Phe Asp Ile Glu Gly Cys Pro Val Pro Gly Pro Thr Phe Cys Pro Ser
      205                      210                      215

aac cct cat aat tgg tgg gaa ggt tat gcc tat cag tct ctt aac gcc      1061
Asn Pro His Asn Trp Trp Glu Gly Tyr Ala Tyr Gln Ser Leu Asn Ala
      220                      225                      230

gtt gaa gct cga cgt tac cgg tgg gtt aga gta aac cat atg gtt tat      1109
Val Glu Ala Arg Arg Tyr Arg Trp Val Arg Val Asn His Met Val Tyr
      240                      245                      250

gat tat tgt act gac cgg tct agg ttt cct gtc cca cca ccc gag tgt      1157
Asp Tyr Cys Thr Asp Arg Ser Arg Phe Pro Val Pro Pro Pro Glu Cys
      255                      260                      265

cgt gct tga aaataattgc atacgtacgt tgcaatgatc atgt                      1200
Arg Ala
      270

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<210> 116

<211> 269

<212> PRT

<213> Arabidopsis thaliana

<400> 116

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Met Phe Ile Arg Val Ser Ala Arg Pro Ala Thr Phe Val Glu Asp Phe
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Lys Ala Ala Trp Ser Glu Ser His Ile Arg Gln Met Glu Asp Gly Lys
      20                      25                      30

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Ala Ile Gln Leu Val Leu Asp Gln Ser Thr Gly Cys Gly Phe Ala Ser
      35                      40                      45

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220

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Lys Arg Lys Tyr Leu Phe Gly Arg Val Ser Met Lys Ile Lys Leu Ile
  50          55          60
Pro Gly Asp Ser Ala Gly Thr Val Thr Ala Phe Tyr Met Asn Ser Asp
  65          70          75          80
Thr Ala Thr Val Arg Asp Glu Leu Asp Phe Glu Phe Leu Gly Asn Arg
          85          90          95
Ser Gly Gln Pro Tyr Ser Val Gln Thr Asn Ile Phe Ala His Gly Lys
          100          105          110
Gly Asp Arg Glu Gln Arg Val Asn Leu Trp Phe Asp Pro Ser Met Asp
          115          120          125
Tyr His Thr Tyr Thr Ile Leu Trp Ser His Lys His Ile Val Phe Tyr
          130          135          140
Val Asp Asp Val Pro Ile Arg Glu Tyr Lys Asn Asn Glu Ala Lys Asn
          145          150          155          160
Ile Ala Tyr Pro Thr Ser Gln Pro Met Gly Val Tyr Ser Thr Leu Trp
          165          170          175
Glu Ala Asp Asp Trp Ala Thr Arg Gly Gly Leu Glu Lys Ile Asp Trp
          180          185          190
Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr Lys Asp Phe Asp Ile Glu Gly
          195          200          205
Cys Pro Val Pro Gly Pro Thr Phe Cys Pro Ser Asn Pro His Asn Trp
          210          215          220
Trp Glu Gly Tyr Ala Tyr Gln Ser Leu Asn Ala Val Glu Ala Arg Arg
          225          230          235          240
Tyr Arg Trp Val Arg Val Asn His Met Val Tyr Asp Tyr Cys Thr Asp
          245          250          255
Arg Ser Arg Phe Pro Val Pro Pro Pro Glu Cys Arg Ala
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<220>
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<400> 117

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                        1                      5

atc cgc aga acc cta acc aaa cca cac ggc act ttt tcc cgg tgt cgc      99
Ile Arg Arg Thr Leu Thr Lys Pro His Gly Thr Phe Ser Arg Cys Arg
10                      15                      20                      25

tac tta tca acc gcc gct gct gcg acg gag gtg aat tac gag gat gaa      147
Tyr Leu Ser Thr Ala Ala Ala Ala Thr Glu Val Asn Tyr Glu Asp Glu
                      30                      35                      40

tcg att atg atg aaa gga gtt cga att tca ggt aga cct ctt tac tta      195
Ser Ile Met Met Lys Gly Val Arg Ile Ser Gly Arg Pro Leu Tyr Leu
                      45                      50                      55

gat atg caa gcg acg act ccg att gat cct aga gta ttc gat gcg atg      243
Asp Met Gln Ala Thr Thr Pro Ile Asp Pro Arg Val Phe Asp Ala Met
                      60                      65                      70

aat gct tca cag atc cat gag tat ggg aat cct cac tcg cga acg cat      291
Asn Ala Ser Gln Ile His Glu Tyr Gly Asn Pro His Ser Arg Thr His
                      75                      80                      85

ctc tac ggc tgg gaa gct gag aac gcc gtc gag aac gca cga aac cag      339
Leu Tyr Gly Trp Glu Ala Glu Asn Ala Val Glu Asn Ala Arg Asn Gln
                      90                      95                      100                      105

gtc gcg aaa ctg atc gaa gct tca ccg aag gag atc gta ttc gtg tcc      387
Val Ala Lys Leu Ile Glu Ala Ser Pro Lys Glu Ile Val Phe Val Ser
                      110                      115                      120

ggg gca acg gag gcg aac aat atg gcg gtg aaa gga gtg atg cac ttt      435
Gly Ala Thr Glu Ala Asn Asn Met Ala Val Lys Gly Val Met His Phe
                      125                      130                      135

tac aag gac acg aag aaa cat gtg ata act aca cag act gag cat aag      483
Tyr Lys Asp Thr Lys Lys His Val Ile Thr Thr Gln Thr Glu His Lys
                      140                      145                      150

tgt gtg ctt gat tcg tgt agg cat ttg cag caa gaa gga ttt gag gta      531
Cys Val Leu Asp Ser Cys Arg His Leu Gln Gln Glu Gly Phe Glu Val
                      155                      160                      165

act tat tta cct gtg aaa act gat gga ttg gtt gat tta gag atg ttg      579
Thr Tyr Leu Pro Val Lys Thr Asp Gly Leu Val Asp Leu Glu Met Leu
                      170                      175                      180                      185

aga gaa gct att agg cca gac aca ggg cta gtt tct att atg gct gtg      627
Arg Glu Ala Ile Arg Pro Asp Thr Gly Leu Val Ser Ile Met Ala Val
                      190                      195                      200

aac aat gag att ggt gtg gtt caa cct atg gag gag att ggt atg att      675
Asn Asn Glu Ile Gly Val Val Gln Pro Met Glu Glu Ile Gly Met Ile
                      205                      210                      215

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tgc aaa gag cat aat gtt ccg ttt cat act gat gct gct caa gct att	723
Cys Lys Glu His Asn Val Pro Phe His Thr Asp Ala Ala Gln Ala Ile	
220 225 230	
ggg aag ata cct gtt gat gtt aag aag tgg aat gtt gct ttg atg tct	771
Gly Lys Ile Pro Val Asp Val Lys Lys Trp Asn Val Ala Leu Met Ser	
235 240 245	
atg agt gct cac aag atc tat gga ccg aaa ggt gtt ggt gct ttg tat	819
Met Ser Ala His Lys Ile Tyr Gly Pro Lys Gly Val Gly Ala Leu Tyr	
250 255 260 265	
gtg agg agg agg ccg aga atc agg ctt gag ccg ttg atg aat ggt gga	867
Val Arg Arg Arg Pro Arg Ile Arg Leu Glu Pro Leu Met Asn Gly Gly	
270 275 280	
ggg cag gag agg gga ttg cgt agt ggt acg ggg gct acg cag cag att	915
Gly Gln Glu Arg Gly Leu Arg Ser Gly Thr Gly Ala Thr Gln Gln Ile	
285 290 295	
gtt ggg ttc ggg gct gct tgt gag ttg gct atg aag gag atg gag tat	963
Val Gly Phe Gly Ala Ala Cys Glu Leu Ala Met Lys Glu Met Glu Tyr	
300 305 310	
gat gag aag tgg att aag ggg tta cag gag agg ttg ctg aat ggg gtt	1011
Asp Glu Lys Trp Ile Lys Gly Leu Gln Glu Arg Leu Leu Asn Gly Val	
315 320 325	
aga gag aag ctt gat ggt gtt gtg gtg aat ggt tca atg gat agt cga	1059
Arg Glu Lys Leu Asp Gly Val Val Val Asn Gly Ser Met Asp Ser Arg	
330 335 340 345	
tat gta ggg aat ttg aat ttg tcg ttt gct tat gtt gaa gga gag agt	1107
Tyr Val Gly Asn Leu Asn Leu Ser Phe Ala Tyr Val Glu Gly Glu Ser	
350 355 360	
ttg ttg atg gga ttg aag gaa gtt gca gtg tct agt gga agt gct tgt	1155
Leu Leu Met Gly Leu Lys Glu Val Ala Val Ser Ser Gly Ser Ala Cys	
365 370 375	
act agt gcg agt ttg gag cct tct tat gtg ttg aga gct ttg ggt gtg	1203
Thr Ser Ala Ser Leu Glu Pro Ser Tyr Val Leu Arg Ala Leu Gly Val	
380 385 390	
gat gaa gac atg gct cac act tcg att agg ttt ggg att ggt agg ttt	1251
Asp Glu Asp Met Ala His Thr Ser Ile Arg Phe Gly Ile Gly Arg Phe	
395 400 405	
acc acg aag gaa gag att gat aaa gcg gtc gag ctt acg gtt aaa caa	1299
Thr Thr Lys Glu Glu Ile Asp Lys Ala Val Glu Leu Thr Val Lys Gln	
410 415 420 425	
gtt gag aag ttg agg gaa atg agc ccg ctt tat gaa atg gtt aaa gaa	1347
Val Glu Lys Leu Arg Glu Met Ser Pro Leu Tyr Glu Met Val Lys Glu	
430 435 440	
ggg atc gat atc aag aac att caa tgg tct caa cac tga ttcaacagtt	1396

Gly Ile Asp Ile Lys Asn Ile Gln Trp Ser Gln His
 445 450

cca

1399

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<213> Arabidopsis thaliana

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Pro His Gly Thr Phe Ser Arg Cys Arg Tyr Leu Ser Thr Ala Ala Ala
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Ala Thr Glu Val Asn Tyr Glu Asp Glu Ser Ile Met Met Lys Gly Val
 35 40 45

Arg Ile Ser Gly Arg Pro Leu Tyr Leu Asp Met Gln Ala Thr Thr Pro
 50 55 60

Ile Asp Pro Arg Val Phe Asp Ala Met Asn Ala Ser Gln Ile His Glu
 65 70 75 80

Tyr Gly Asn Pro His Ser Arg Thr His Leu Tyr Gly Trp Glu Ala Glu
 85 90 95

Asn Ala Val Glu Asn Ala Arg Asn Gln Val Ala Lys Leu Ile Glu Ala
 100 105 110

Ser Pro Lys Glu Ile Val Phe Val Ser Gly Ala Thr Glu Ala Asn Asn
 115 120 125

Met Ala Val Lys Gly Val Met His Phe Tyr Lys Asp Thr Lys Lys His
 130 135 140

Val Ile Thr Thr Gln Thr Glu His Lys Cys Val Leu Asp Ser Cys Arg
 145 150 155 160

His Leu Gln Gln Glu Gly Phe Glu Val Thr Tyr Leu Pro Val Lys Thr
 165 170 175

Asp Gly Leu Val Asp Leu Glu Met Leu Arg Glu Ala Ile Arg Pro Asp
 180 185 190

Thr Gly Leu Val Ser Ile Met Ala Val Asn Asn Glu Ile Gly Val Val
 195 200 205

Gln Pro Met Glu Glu Ile Gly Met Ile Cys Lys Glu His Asn Val Pro
 210 215 220

Phe His Thr Asp Ala Ala Gln Ala Ile Gly Lys Ile Pro Val Asp Val
 225 230 235 240

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<400> 119

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	Met	Leu	Thr	Asn	Thr	Asn	Leu	Phe	Phe	Phe	Leu	Ser	Leu	Leu		
	1				5					10						
ctt	ctt	tct	tgt	ttt	ctc	caa	gtt	tct	tcc	aat	gga	gac	gct	gag	ata	97
Leu	Leu	Ser	Cys	Phe	Leu	Gln	Val	Ser	Ser	Asn	Gly	Asp	Ala	Glu	Ile	
15					20					25					30	
ttg	agt	aga	gtt	aaa	aag	acc	cga	ctt	ttc	gac	ccc	gat	gga	aat	tta	145
Leu	Ser	Arg	Val	Lys	Lys	Thr	Arg	Leu	Phe	Asp	Pro	Asp	Gly	Asn	Leu	
				35					40					45		
caa	gat	tggt	gtc	ata	acc	gga	gat	aat	cgg	agt	cca	tgt	aat	tggt	acg	193
Gln	Asp	Trp	Val	Ile	Thr	Gly	Asp	Asn	Arg	Ser	Pro	Cys	Asn	Trp	Thr	
			50					55					60			
gga	atc	aca	tgc	cac	atc	aga	aaa	ggg	agc	tcc	ctc	gcc	gtc	act	acc	241
Gly	Ile	Thr	Cys	His	Ile	Arg	Lys	Gly	Ser	Ser	Leu	Ala	Val	Thr	Thr	
	65					70						75				
att	gat	ctc	tcc	ggc	tat	aat	atc	tcc	ggg	ggc	ttt	ccc	tac	gga	ttc	289
Ile	Asp	Leu	Ser	Gly	Tyr	Asn	Ile	Ser	Gly	Gly	Phe	Pro	Tyr	Gly	Phe	
	80					85					90					
tgt	cgt	atc	cgt	aca	ctc	atc	aac	atc	act	ctt	tct	caa	aac	aat	ctc	337
Cys	Arg	Ile	Arg	Thr	Leu	Ile	Asn	Ile	Thr	Leu	Ser	Gln	Asn	Asn	Leu	
95					100					105					110	
aat	ggg	acg	att	gat	tct	gct	cct	ctc	tcc	ctc	tgt	tct	aaa	ctt	cag	385
Asn	Gly	Thr	Ile	Asp	Ser	Ala	Pro	Leu	Ser	Leu	Cys	Ser	Lys	Leu	Gln	
				115					120					125		
aat	ttg	att	ctc	aat	caa	aac	aac	ttc	tcc	ggg	aaa	tta	ccg	gaa	ttc	433
Asn	Leu	Ile	Leu	Asn	Gln	Asn	Asn	Phe	Ser	Gly	Lys	Leu	Pro	Glu	Phe	
			130					135					140			
tca	ccg	gag	ttt	cgt	aaa	tta	cga	gtc	ctc	gaa	ttg	gaa	tca	aac	ctc	481
Ser	Pro	Glu	Phe	Arg	Lys	Leu	Arg	Val	Leu	Glu	Leu	Glu	Ser	Asn	Leu	
		145				150						155				
ttc	acc	ggg	gag	att	cct	caa	agt	tac	ggg	aga	ctc	act	gct	ctg	caa	529
Phe	Thr	Gly	Glu	Ile	Pro	Gln	Ser	Tyr	Gly	Arg	Leu	Thr	Ala	Leu	Gln	
	160					165					170					
gtt	ctg	aat	ctt	aat	ggg	aac	ccg	ctc	agt	gga	atc	gtt	ccg	gcg	ttt	577
Val	Leu	Asn	Leu	Asn	Gly	Asn	Pro	Leu	Ser	Gly	Ile	Val	Pro	Ala	Phe	
175					180					185					190	
ttg	ggg	tat	ctg	act	gag	tta	act	cgt	ctt	gat	ctc	gct	tac	atc	agt	625
Leu	Gly	Tyr	Leu	Thr	Glu	Leu	Thr	Arg	Leu	Asp	Leu	Ala	Tyr	Ile	Ser	
				195					200					205		

ttt gat cct agt ccg att cca tca acc ttg ggg aac ttg tcg aat ctg	673
Phe Asp Pro Ser Pro Ile Pro Ser Thr Leu Gly Asn Leu Ser Asn Leu	
210 215 220	
act gat ctt cgg cta act cac tcg aac ctc gtc gga gaa att cct gat	721
Thr Asp Leu Arg Leu Thr His Ser Asn Leu Val Gly Glu Ile Pro Asp	
225 230 235	
tcg atc atg aat ctg gtg ttg tta gag aat ctt gat tta gct atg aat	769
Ser Ile Met Asn Leu Val Leu Leu Glu Asn Leu Asp Leu Ala Met Asn	
240 245 250	
agt ctc acc gga gaa ata cct gag agt atc gga aga ctc gaa tcg gtt	817
Ser Leu Thr Gly Glu Ile Pro Glu Ser Ile Gly Arg Leu Glu Ser Val	
255 260 265 270	
tac cag att gag ctc tac gat aac cgg tta tct gga aaa tta ccg gag	865
Tyr Gln Ile Glu Leu Tyr Asp Asn Arg Leu Ser Gly Lys Leu Pro Glu	
275 280 285	
agt atc gga aat tta acc gaa ttg agg aat ttt gat gtc tcg cag aat	913
Ser Ile Gly Asn Leu Thr Glu Leu Arg Asn Phe Asp Val Ser Gln Asn	
290 295 300	
aat cta acc ggt gaa cta ccg gaa aag atc gct gct ctg caa ctt atc	961
Asn Leu Thr Gly Glu Leu Pro Glu Lys Ile Ala Ala Leu Gln Leu Ile	
305 310 315	
tct ttc aat ctc aat gat aat ttc ttc acc gga gga tta cca gat gtc	1009
Ser Phe Asn Leu Asn Asp Asn Phe Phe Thr Gly Gly Leu Pro Asp Val	
320 325 330	
gta gct ttg aat cct aat ctc gtt gaa ttc aaa atc ttc aac aac agt	1057
Val Ala Leu Asn Pro Asn Leu Val Glu Phe Lys Ile Phe Asn Asn Ser	
335 340 345 350	
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Phe Thr Gly Thr Leu Pro Arg Asn Leu Gly Lys Phe Ser Glu Ile Ser	
355 360 365	
gaa ttc gat gtc tcg acg aac aga ttc tcc ggt gaa ttg ccg ccg tat	1153
Glu Phe Asp Val Ser Thr Asn Arg Phe Ser Gly Glu Leu Pro Pro Tyr	
370 375 380	
ttg tgc tac aga aga aaa ctt cag aag att atc acc ttc agc aat caa	1201
Leu Cys Tyr Arg Arg Lys Leu Gln Lys Ile Ile Thr Phe Ser Asn Gln	
385 390 395	
tta agc ggc gaa att ccg gaa tct tac ggc gat tgt cat tcg ctt aat	1249
Leu Ser Gly Glu Ile Pro Glu Ser Tyr Gly Asp Cys His Ser Leu Asn	
400 405 410	
tac att cgt atg gcg gat aac aaa ctc tcc ggc gaa gtt ccg gct agg	1297
Tyr Ile Arg Met Ala Asp Asn Lys Leu Ser Gly Glu Val Pro Ala Arg	
415 420 425 430	
ttt tgg gaa ctt cct ctt act cgt ctt gag cta gcc aac aac aat caa	1345

Phe Trp Glu Leu Pro Leu Thr Arg Leu Glu Leu Ala Asn Asn Asn Gln	
435 440 445	
tta caa ggt tgc att cct cct tgc att tcc aaa gct cgt cat cta tct	1393
Leu Gln Gly Ser Ile Pro Pro Ser Ile Ser Lys Ala Arg His Leu Ser	
450 455 460	
cag ctt gaa atc tcc gct aac aac ttc tcc ggt gtg att ccc gtc aaa	1441
Gln Leu Glu Ile Ser Ala Asn Asn Phe Ser Gly Val Ile Pro Val Lys	
465 470 475	
ctt tgt gat ctc cgt gat ctc aga gtc atc gat ctt agc cgc aac agt	1489
Leu Cys Asp Leu Arg Asp Leu Arg Val Ile Asp Leu Ser Arg Asn Ser	
480 485 490	
ttc tta gga tca att ccg tct tgc atc aac aaa ttg aag aat cta gag	1537
Phe Leu Gly Ser Ile Pro Ser Cys Ile Asn Lys Leu Lys Asn Leu Glu	
495 500 505 510	
aga gta gag atg cag gag aac atg ctc gac ggc gag att ccg agt tca	1585
Arg Val Glu Met Gln Glu Asn Met Leu Asp Gly Glu Ile Pro Ser Ser	
515 520 525	
gtg agt tgc tgc acc gag tta acc gaa tta aat ctc tcc aac aac cgt	1633
Val Ser Ser Cys Thr Glu Leu Thr Glu Leu Asn Leu Ser Asn Asn Arg	
530 535 540	
tta cga ggc ggg ata cca ccg gaa ctc ggt gat tta ccg gtt tta aac	1681
Leu Arg Gly Gly Ile Pro Pro Glu Leu Gly Asp Leu Pro Val Leu Asn	
545 550 555	
tac ctg gat ctc tct aac aac caa ctc acc ggt gag att ccg gcg gag	1729
Tyr Leu Asp Leu Ser Asn Asn Gln Leu Thr Gly Glu Ile Pro Ala Glu	
560 565 570	
ctg ttg agg ctc aag ctt aat caa ttc aac gtc tcc gat aac aaa ctc	1777
Leu Leu Arg Leu Lys Leu Asn Gln Phe Asn Val Ser Asp Asn Lys Leu	
575 580 585 590	
tat g gtaagattcc ttctggattt cagcaagata tttttcgacc cagttttctta g gt	1834
Tyr G ly	
aac ccg aat ctc tgt gcc cca aat ttg gat ccg att aga cct tgc cga	1882
Asn Pro Asn Leu Cys Ala Pro Asn Leu Asp Pro Ile Arg Pro Cys Arg	
595 600 605	
tcc aaa cgg gaa acc cgg tac att ctc cca atc tca atc ctc tgc atc	1930
Ser Lys Arg Glu Thr Arg Tyr Ile Leu Pro Ile Ser Ile Leu Cys Ile	
610 615 620	
gtt gca cta acc gga gct ttg gtt tgg cta ttc atc aaa acc aaa ccg	1978
Val Ala Leu Thr Gly Ala Leu Val Trp Leu Phe Ile Lys Thr Lys Pro	
625 630 635 640	
tta ttc aag aga aaa ccg aaa cgg acc aac aaa ata acc atc ttc cag	2026
Leu Phe Lys Arg Lys Pro Lys Arg Thr Asn Lys Ile Thr Ile Phe Gln	
645 650 655	

cgg gtc ggg ttc acg gag gaa gac ata tac ccg caa tta aca gaa gat	2074
Arg Val Gly Phe Thr Glu Glu Asp Ile Tyr Pro Gln Leu Thr Glu Asp	
660 665 670	
aac ata att ggg tcg ggc ggg tcg ggt ttg gtt tat aga gtg aaa ctc	2122
Asn Ile Ile Gly Ser Gly Gly Ser Gly Leu Val Tyr Arg Val Lys Leu	
675 680 685	
aaa tca ggt caa acg ctt gcg gtg aag aaa ctc tgg gga gaa acg ggt	2170
Lys Ser Gly Gln Thr Leu Ala Val Lys Lys Leu Trp Gly Glu Thr Gly	
690 695 700	
caa aaa acg gaa tct gaa tct gtt ttt cga tcc gaa gta gag acg ttg	2218
Gln Lys Thr Glu Ser Glu Ser Val Phe Arg Ser Glu Val Glu Thr Leu	
705 710 715 720	
ggt cgg gtc aga cat gga aac atc gtg aaa ctt ctt atg tgc tgc aac	2266
Gly Arg Val Arg His Gly Asn Ile Val Lys Leu Leu Met Cys Cys Asn	
725 730 735	
ggc gag gag ttt cgg ttc tta gtg tac gag ttc atg gaa aac ggc agc	2314
Gly Glu Glu Phe Arg Phe Leu Val Tyr Glu Phe Met Glu Asn Gly Ser	
740 745 750	
tta ggt gac gtt ttg cat tcg gag aaa gaa cat cgt gcc gtt tct cca	2362
Leu Gly Asp Val Leu His Ser Glu Lys Glu His Arg Ala Val Ser Pro	
755 760 765	
ctt gat tgg acg aca cga ttt tcg atc gcg gtt ggt gct gct caa gga	2410
Leu Asp Trp Thr Thr Arg Phe Ser Ile Ala Val Gly Ala Ala Gln Gly	
770 775 780	
ctt tct tat cta cat cat gac tct gtt ccg cct att gtt cac cgt gac	2458
Leu Ser Tyr Leu His His Asp Ser Val Pro Pro Ile Val His Arg Asp	
785 790 795 800	
gtc aaa agc aat aat ata ttg ttg gac cat gag atg aag cca cgt gtc	2506
Val Lys Ser Asn Asn Ile Leu Leu Asp His Glu Met Lys Pro Arg Val	
805 810 815	
gcc gat ttc ggt tta gct aaa ccg ttg aag aga gaa gac aat gat ggt	2554
Ala Asp Phe Gly Leu Ala Lys Pro Leu Lys Arg Glu Asp Asn Asp Gly	
820 825 830	
gtc tcc gat gtt tca atg tct tgt gtt gct gga tcc tac ggc tac att	2602
Val Ser Asp Val Ser Met Ser Cys Val Ala Gly Ser Tyr Gly Tyr Ile	
835 840 845	
gct ccg g gttcgaattc ttagctctac aatatcaaat cgtaaacc ctatacgcaa	2659
Ala Pro G	
850	
gcgttttagt aacattactg ttcttctgtg gatgcag aa tat ggt tat acg tca	2713
lu Tyr Gly Tyr Thr Ser	
855	

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aaa gtg aat gag aag agc gat gtc tat agc ttc ggg gtg gtt tta ctc 2761
Lys Val Asn Glu Lys Ser Asp Val Tyr Ser Phe Gly Val Val Leu Leu
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gaa ctg att acg gga aaa aga ccg aac gat tcg tct ttt ggg gag aat 2809
Glu Leu Ile Thr Gly Lys Arg Pro Asn Asp Ser Ser Phe Gly Glu Asn
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aag gac att gtt aag ttt gca atg gaa gca gct ttg tgt tac cct tct 2857
Lys Asp Ile Val Lys Phe Ala Met Glu Ala Ala Leu Cys Tyr Pro Ser
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cca tca gca gaa gac gga gcc atg aat caa gat tca ctt gga aac tat 2905
Pro Ser Ala Glu Asp Gly Ala Met Asn Gln Asp Ser Leu Gly Asn Tyr
905                        910                        915                        920

cga gat ctt agc aag ctt gtt gat cca aag atg aaa ctt tcg acg aga 2953
Arg Asp Leu Ser Lys Leu Val Asp Pro Lys Met Lys Leu Ser Thr Arg
                        925                        930                        935

gag tat gaa gag ata gag aaa gtt ctt gac gtt gca ttg ctc tgt acg 3001
Glu Tyr Glu Glu Ile Glu Lys Val Leu Asp Val Ala Leu Leu Cys Thr
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tcg tct ttt cct atc aac agg ccg acc atg agg aaa gta gta gag ttg 3049
Ser Ser Phe Pro Ile Asn Arg Pro Thr Met Arg Lys Val Val Glu Leu
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ctt aaa gag aag aaa tca cta gag tga tattaatcct aggcttttaa 3096
Leu Lys Glu Lys Lys Ser Leu Glu
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Arg Val Lys Lys Thr Arg Leu Phe Asp Pro Asp Gly Asn Leu Gln Asp
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Trp Val Ile Thr Gly Asp Asn Arg Ser Pro Cys Asn Trp Thr Gly Ile
50                55                60

Thr Cys His Ile Arg Lys Gly Ser Ser Leu Ala Val Thr Thr Ile Asp
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Leu Ser Gly Tyr Asn Ile Ser Gly Gly Phe Pro Tyr Gly Phe Cys Arg
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 Ile Arg Thr Leu Ile Asn Ile Thr Leu Ser Gln Asn Asn Leu Asn Gly
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 Ile Leu Asn Gln Asn Asn Phe Ser Gly Lys Leu Pro Glu Phe Ser Pro
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 Glu Phe Arg Lys Leu Arg Val Leu Glu Leu Glu Ser Asn Leu Phe Thr
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 Gly Glu Ile Pro Gln Ser Tyr Gly Arg Leu Thr Ala Leu Gln Val Leu
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 Asn Leu Asn Gly Asn Pro Leu Ser Gly Ile Val Pro Ala Phe Leu Gly
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 Tyr Leu Thr Glu Leu Thr Arg Leu Asp Leu Ala Tyr Ile Ser Phe Asp
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 Pro Ser Pro Ile Pro Ser Thr Leu Gly Asn Leu Ser Asn Leu Thr Asp
 210 215 220
 Leu Arg Leu Thr His Ser Asn Leu Val Gly Glu Ile Pro Asp Ser Ile
 225 230 235 240
 Met Asn Leu Val Leu Leu Glu Asn Leu Asp Leu Ala Met Asn Ser Leu
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 260 265 270
 Ile Glu Leu Tyr Asp Asn Arg Leu Ser Gly Lys Leu Pro Glu Ser Ile
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 Thr Gly Glu Leu Pro Glu Lys Ile Ala Ala Leu Gln Leu Ile Ser Phe
 305 310 315 320
 Asn Leu Asn Asp Asn Phe Phe Thr Gly Gly Leu Pro Asp Val Val Ala
 325 330 335
 Leu Asn Pro Asn Leu Val Glu Phe Lys Ile Phe Asn Asn Ser Phe Thr
 340 345 350
 Gly Thr Leu Pro Arg Asn Leu Gly Lys Phe Ser Glu Ile Ser Glu Phe
 355 360 365
 Asp Val Ser Thr Asn Arg Phe Ser Gly Glu Leu Pro Pro Tyr Leu Cys
 370 375 380

Tyr Arg Arg Lys Leu Gln Lys Ile Ile Thr Phe Ser Asn Gln Leu Ser
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 Gly Glu Ile Pro Glu Ser Tyr Gly Asp Cys His Ser Leu Asn Tyr Ile
 405 410 415
 Arg Met Ala Asp Asn Lys Leu Ser Gly Glu Val Pro Ala Arg Phe Trp
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 Glu Leu Pro Leu Thr Arg Leu Glu Leu Ala Asn Asn Asn Gln Leu Gln
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 Gly Ser Ile Pro Pro Ser Ile Ser Lys Ala Arg His Leu Ser Gln Leu
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 Glu Ile Ser Ala Asn Asn Phe Ser Gly Val Ile Pro Val Lys Leu Cys
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 Asp Leu Arg Asp Leu Arg Val Ile Asp Leu Ser Arg Asn Ser Phe Leu
 485 490 495
 Gly Ser Ile Pro Ser Cys Ile Asn Lys Leu Lys Asn Leu Glu Arg Val
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 Glu Met Gln Glu Asn Met Leu Asp Gly Glu Ile Pro Ser Ser Val Ser
 515 520 525
 Ser Cys Thr Glu Leu Thr Glu Leu Asn Leu Ser Asn Asn Arg Leu Arg
 530 535 540
 Gly Gly Ile Pro Pro Glu Leu Gly Asp Leu Pro Val Leu Asn Tyr Leu
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 Asp Leu Ser Asn Asn Gln Leu Thr Gly Glu Ile Pro Ala Glu Leu Leu
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 Arg Leu Lys Leu Asn Gln Phe Asn Val Ser Asp Asn Lys Leu Tyr Gly
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 Asn Pro Asn Leu Cys Ala Pro Asn Leu Asp Pro Ile Arg Pro Cys Arg
 595 600 605
 Ser Lys Arg Glu Thr Arg Tyr Ile Leu Pro Ile Ser Ile Leu Cys Ile
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 Val Ala Leu Thr Gly Ala Leu Val Trp Leu Phe Ile Lys Thr Lys Pro
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 Leu Phe Lys Arg Lys Pro Lys Arg Thr Asn Lys Ile Thr Ile Phe Gln
 645 650 655
 Arg Val Gly Phe Thr Glu Glu Asp Ile Tyr Pro Gln Leu Thr Glu Asp
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 Asn Ile Ile Gly Ser Gly Gly Ser Gly Leu Val Tyr Arg Val Lys Leu
 675 680 685

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 930 935 940
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